O-Superfamily Conotoxin Peptides

McIntosh, J. Michael Layer, Richard T. Jones, Robert M.

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AUG 2 n 2001

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2000-12-28 US 60/243,412 2000-10-27

2314-227

US 09/749,637

US60/219,440 2000-07-20 <150> US 60/214,263

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gtc aag ccg tgc cgt aaa gaa ggt caa ctt tgt gat ccg ata ttt caa 192 Val Lys Pro Cys Arg Lys Glu Gly Gln Leu Cys Asp Pro Ile Phe Gln 50

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Gln Leu Cys Asp Pro Ile Phe Gln Asn Cys Cys His Gly Leu Phe Cys
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Val Leu Val Cys Val
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Cys Hi	s Gly	Leu 20	Phe	Cys	Val	Leu	Val 25	Cys	Val							
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aac ct Asn Le															195	
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 Arg His Gln Glu Arg Pro Asp Thr Gly Asp Lys Glu Glu Met Leu Leu
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 aac tgc tgc agt ggt tat aat tgc atc att ttt ttc tgc cta
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Phe	Pro	Lys 35	Ala	Arg	His	Glu	Met 40	Glu	Asn	Leu	Glu	Asp 45	Ser	Lys	His		
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	00> L Ly:	20 s Xaa	Cys	Ser 5	Xaa	Xaa	Gly	Gln	Leu 10	Cys	Asp	Xaa	Leu	Ser 15	Gln	
Ası	п Су	s Cys	Arg 20	Gly	Xaa	His	Cys	Val 25	Leu	Val	Ser	Cys	Val 30			
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 Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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 Gln Asn Cys Cys Asp Gly Tyr Cys Ile Val Leu Val Cys Thr
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<213>
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<220>
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<222>
       (1)..(27)
       Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 7 may be
        Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr, 125-I-Ty
       r, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
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Cys Asp Gly Xaa Cys Ile Val Leu Val Cys Thr
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       DNA
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<220>
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tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt
                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                            40
aac aag agg tgg tgc aaa caa agc ggt gaa atg tgt aat ttg tta gac
                                                                      192
Asn Lys Arg Trp Cys Lys Gln Ser Gly Glu Met Cys Asn Leu Leu Asp
                        55
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caa aac tgc tgc gag ggc tat tgc ata gta ctt gtc tgc aca
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 Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
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Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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Gln Asn Cys Cys Glu Gly Tyr Cys Ile Val Leu Val Cys Thr
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        8 may be Glu or gamma-carboxy-Glu; Xaa at residue 20 may be Tyr,
        125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
        -Tyr
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Cys Xaa Gly Xaa Cys Ile Val Leu Val Cys Thr
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                                                                           48
tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ctt
                                                                           96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
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ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct aag ttg aat
                                                                     144
Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
                            40
                                                                     192
gag agg tgc ctt ggt ggt ggt gaa gtt tgt gat atc ttt ttt cca caa
Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Pro Gln
                        55
tgc tgt ggc tat tgc att ctt ctt ttc tgc aca taaaactacc gtgatgtctt
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Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
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ctcctcccct c
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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
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Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
Glu Arg Cys Leu Gly Gly Gly Glu Val Cys Asp Ile Phe Phe Pro Gln
Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Thr
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<213> Conus dalli
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<221> SITE
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      (1)..(25)
      Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
       13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I-
       Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
<400> 37
Cys Leu Gly Gly Kaa Val Cys Asp Ile Phe Phe Xaa Gln Cys Cys
Gly Xaa Cys Ile Leu Leu Phe Cys Thr
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      (70)..(300)
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atc	gcca	ag a M 1	let L	aa c ys L	tg a eu T	cg t hr C	ys M	itg a let N	atg a Met]	atc g [le V	al A	rct g la V .0	rtg c 'al I	etg t Jeu E	tc Phe	ttg Leu	111
acc Thr 15	gcc Ala	tgg Trp	aca Thr	ttt Phe	gcc Ala 20	acg Thr	gct Ala	gat Asp	gac Asp	c ccc Pro 25	aga Arg	. aat Asn	gga Gly	ı tt <u>o</u> Lev	g gg 30	y g	159
aat Asn	att Ile	ttt Phe	tcg Ser	aat Asn 35	gca Ala	cat His	cac His	gaa Glu	atç Met 40	j aag : Lys	aat Asn	ccc Pro	gaa Glu	gcc Ala 45	tc Se	t r	207
aaa Lys	ttg Leu	aac Asn	aag Lys 50	agg Arg	tgc Cys	cgt Arg	cta Leu	ggg Gly 55	gct Ala	gaa Glu	agt Ser	tgt Cys	gat Asp 60	gta Val	at Il	t e	255
tca Ser	caa Gln	aac Asn 65	tgc Cys	tgc Cys	caa Gln	ggc Gly	acg Thr 70	tgc Cys	gtt Val	ttt Phe	ttc Phe	tgc Cys 75	tta Leu	cca Pro			300
tgat	gtc	ttc	tatt	ctcct	c to	gtgc	tacc	t gg	cttg	atct	ttc	atta	gcg	cgtg	cctt	tc	360
actg	gtt	atg	aacc	ccct	ga to	ccga	ctct	c tg	gcag	cctc	ggg	ggtt	caa	catc	caaa	ata	420
aaac	gac	agc a	acaat	tgaca	aa a												441
<210 <211 <212 <213	> '	39 77 PRT Conus	s glo	oriam	naris	5											
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Trp	Thr	Phe	Ala 20	Thr	Ala	Asp	Asp	Pro 25	Arg	Asn	Gly	Leu	Gly 30	Asn	Ile)	
Phe	Ser	Asn 35	Ala	His	His	Glu	Met 40	Lys	Asn	Pro	Glu	Ala 45	Ser	Lys	Let	1	
Asn :	Lys 50	Arg	Cys	Arg	Leu	Gly 55	Ala	Glu	Ser	Cys	Asp 60	Val	Ile	Ser	Gln	L	
Asn (65	Cys	Cys	Gln	Gly	Thr 70	Cys	Val	Phe	Phe	Cys 75	Leu	Pro					
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<220: <221: <222: <223:	> S > (> X	ITE 1) aa a 6 ma	t re	sidu Pro	e 6 or	may hydr	be G	Glu d	or ga	amma-	carb	oxy-	·Glu;	Xaa	ı at	resid	due
<400> Cys <i>I</i> 1		0 Leu	Gly .	Ala : 5	Xaa	Ser	Cys	Asp	Val 10	Ile	Ser	Gln	Asn	Cys 15	Cys		

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                                                                      109
               Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu
ttc ttg acc gcc tgg aca ttc gcc acg gct gat gac ccc aga aat gga
                                                                      157
Phe Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly
        15
                            20
ttq gag aaa ctt ttt tcg aat aca cat cac gaa atg aag aac ccc gaa
                                                                      205
Leu Glu Lys Leu Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu
    30
                        35
gcc tct aaa ttg aac aag agg tgc aaa caa gct gat gaa tct tgt aat
                                                                      253
Ala Ser Lys Leu Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn
                    50
gta ttt tca ctt gac tgc tgc acc ggc tta tgc ttg gga ttc tgc gta
                                                                      301
Val Phe Ser Leu Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val
tcq tgatgtcttc tactcccctc tgtgctacct ggcttgatct ttgattggcg
                                                                      354
Ser
tgtgcctttc attggttatg aaccccctg atccgattct ttggcggcct cgggggttca
                                                                      414
acatccaaat aaagcgacag cacaataaaa aa
                                                                      446
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Phe Ser Asn Thr His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Cys Lys Gln Ala Asp Glu Ser Cys Asn Val Phe Ser Leu
Asp Cys Cys Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
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       PRT
<213>
      Conus gloriamaris
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       Xaa at residue 6 may be Glu or gamma-carboxy-Glu.
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Thr Gly Leu Cys Leu Gly Phe Cys Val Ser
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       DNA
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tgg aca ttc gcc acg gcc atc acc agg aat gga ttg ggg aat ctt ttt
                                                                       96
Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
            20
ccg aag aat cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg aac
                                                                      144
Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
aag agg tgc gtt cca tac gag ggc cct tgt aat tgg ctt aca caa aac
                                                                      192
Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
tgc tgc gat gag cta tgc gta ttt ttc tgc cta taaaactagc ctgatgt
                                                                      242
Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
                    70
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<211>
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<213>
      Conus gloriamaris
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Trp Thr Phe Ala Thr Ala Ile Thr Arg Asn Gly Leu Gly Asn Leu Phe
Pro Lys Asn His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu Asn
Lys Arg Cys Val Pro Tyr Glu Gly Pro Cys Asn Trp Leu Thr Gln Asn
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Cys Cys Asp Glu Leu Cys Val Phe Phe Cys Leu
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       25
<212>
       PRT
       Conus gloriamaris
<220>
<221>
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<222>
       (1)..(25)
<223>
       Xaa at residue 2 and 7 may be Pro or hydroxy-Pro; Xaa at residue
       4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
        or O-phospho-Tyr; Xaa at residue 5 and 18 may be Glu or gamma-ca
       rboxy-Glu ; Xaa at residue 10 may be Trp or bromo-Trp
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tgg aca ttc gcc acg gct gat gac tcc gga aat gga ttg gag aaa ctt
                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Gly Asn Gly Leu Glu Lys Leu
ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
aac aag agg tgc aaa caa gct gat gaa cct tgt gat gta ttt tca ctt
                                                                      192
Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
gaa tgc tgc acc ggc ata tgt ctt gga ttc tgc acg tgg tgatgtcttc
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Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
cctcccctc
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<213> Conus magus
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Asn Lys Arg Cys Lys Gln Ala Asp Glu Pro Cys Asp Val Phe Ser Leu
Glu Cys Cys Thr Gly Ile Cys Leu Gly Phe Cys Thr Trp
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       49
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       26
<212>
      PRT
<213> Conus magus
<220>
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      SITE
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       (1)..(26)
       Xaa at residue 6 and 14 may be Glu or gamma-carboxy-Glu; Xaa at r
       esidue 7 may be Pro or hydroxy-Pro; Xaa at residue 26may be Trp o
       r bromo-Trp
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Thr Gly Ile Cys Leu Gly Phe Cys Thr Xaa
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       DNA
<213>
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                                                                      109
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           Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe
                                                                      157
ttg acc gcc tgg aca ttc gcc acg gct gat gac tcc agc aat gga ttg
Leu Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu
                        20
                                                                       205
gag aat ctt ttt ttg aag gca cat cac gaa atg aac ccc gaa gcc tct
Glu Asn Leu Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser
                    35
                                         40
aag ttg aac gag agg tgc ctt gat gct ggt gaa gtt tgt gat att ttt
                                                                       253
Lys Leu Asn Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe
ttt cca aca tgc tgc ggc tat tgc att ctt ctt ttc tgc gca
                                                                       295
Phe Pro Thr Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
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<211> 26

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gcgtaccctt cactggttat gaaacccctg atccagctct ctggaggcct cgggggttca
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acatccaaat aaagcgaca
<210>
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Phe Leu Lys Ala His His Glu Met Asn Pro Glu Ala Ser Lys Leu Asn
Glu Arg Cys Leu Asp Ala Gly Glu Val Cys Asp Ile Phe Phe Pro Thr
Cys Cys Gly Tyr Cys Ile Leu Leu Phe Cys Ala
                    70
<210>
       52
<211>
       25
<212>
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<213> Conus textile
<220>
<221>
       SITE
<222>
       (1)..(25)
       Xaa at residue 6 may be Glu or gamma-carboxy-Glu; Xaa at residue
       13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-
       I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr.
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Gly Xaa Cys Ile Leu Leu Phe Cys Ala
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       53
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       26
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<221>
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       (1)..(26)
       Xaa at residues 3 and 9 may be Glu or gamma-carboxy-Glu; Xaa at r
       esidue 7 may be Pro or hydroxy-Pro
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 Val Gly Val Cys Phe Leu Met Ala Cys Ile
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      Xaa at residues 3, 7 and 13 may be Pro or hydroxy-Pro; Xaa at re
       sidue 19 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sul
       pho-Tyr or O-phospho-Tyr
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Asn Ser Xaa Cys Val Gln Phe Ile Cys Leu
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
                                     10
tgg aca ttc gcc acg gct gat gac ccc aga aat gga ttg gag aat ttt
                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
            20
ttt tcg aag aca caa cac gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                             40
                                                 45
aac aag agg tgc cta gca gaa cat gaa act tgt aat ata ttt aca caa
                                                                      192
Asn Lys Arg Cys Leu Ala Glu His Glu Thr Cys Asn Ile Phe Thr Gln
aac tgc tgc gaa ggc gtg tgc att ttt atc tgc gta caa gct cca gag
                                                                      240
Asn Cys Cys Glu Gly Val Cys Ile Phe Ile Cys Val Gln Ala Pro Glu
                                         75
                                                                      260
tgatgtcttc tcctcccctc
 <210> 56
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 <212> PRT
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 Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Phe
 Phe Ser Lys Thr Gln His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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                        55
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       Xaa at residue 28 may be Pro or hydroxy-Pro
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Xaa Gly Val Cys Ile Phe Ile Cys Val Gln Ala Xaa Xaa
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                                     10
tgg aca ttt gcc acg gct gaa gac ccc aga cat gga ttg gag aat ctt
                                                                        96
Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg His Gly Leu Glu Asn Leu
                                                                       144
ttt tcg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
                                                 45
         35
gac aag agg tgc att cca cat ttt gac cct tgt gac ccg ata cgc cac
                                                                       192
Asp Lys Arg Cys Ile Pro His Phe Asp Pro Cys Asp Pro Ile Arg His
    50
 ace tge tge ttt gge etg tge eta eta ata gee tge ate taaaaetgee
                                                                       241
 Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Āla Cys Ile
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 gtgatgtctt ctctcccatc
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Thr Cys Cys Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
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       Xaa at residues 3, 7 and 10 may be Pro or hydroxy-Pro.
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Phe Gly Leu Cys Leu Leu Ile Ala Cys Ile
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Met Lys Leu Thr Cys Val Met Thr Val Ala Val Leu Phe Leu Thr Ala
                                                                           48
                                                                           96
tgg aca ttc gtc acg gct gaa gac ccc aga gat gga ttg aag aat ctt
Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Lys Asn Leu
tta tca aat gca cat aac gaa atg aag aac ccc gaa gcc tct aca ttg
                                                                          144
Leu Ser Asn Ala His Asn Glu Met Lys Asn Pro Glu Ala Ser Thr Leu
 aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt ata ctt tat tca
                                                                          192
 Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
 gac tgc tgc ggc tat tgc gtt ggt gct atc tgc cta taaaactacc
                                                                          238
 Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
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Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Ile Leu Tyr Ser
Asp Cys Cys Gly Tyr Cys Val Gly Ala Ile Cys Leu
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       12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
       ulpho-Tyr or O-phospho-Tyr
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Gly Xaa Cys Val Gly Ala Ile Cys Leu
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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
 ttt tcg aag aca caa cac aaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
 Phe Ser Lys Thr Gln His Lys Met Lys Asn Pro Glu Ala Ser Lys Leu
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 aac aag agg tgc aaa gca gaa aat gaa ctt tgt aat ata ttt ata caa
                                                                      192
 Asn Lys Arg Cys Lys Ala Glu Asn Glu Leu Cys Asn Ile Phe Ile Gln
 aac tgc tgc gac ggg acg tgc ctt ctt atc tgc ata caa aat cca cag
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       sidue 28 may be Pro or hydroxy-Pro
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Asp Gly Thr Cys Leu Leu Ile Cys Ile Gln Asn Xaa Gln
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tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg gat aat cgt
                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Asp Asn Arg
ttt tcg aag gca cgt cac gaa atg aat aac cgc aga gcc tct aaa ttg
                                                                     144
Phe Ser Lys Ala Arg His Glu Met Asn Asn Arg Arg Ala Ser Lys Leu
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Phe Ser L	ys Ala 85	Arg His	Glu Me 40		Asn	Arg	Arg	Ala 45	Ser	Lys	Leu	
Asn Lys A 50	arg Cys	Leu Glu	Phe Gl 55	y Glu	Leu	Cys	Asn 60	Phe	Phe	Phe	Pro	
Thr Cys C	Cys Gly	Tyr Cys	Val Le	u Leu	Val	Cys 75	Leu					
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Gly Xaa C	Cys Val 20	Leu Leu	Val Cy	s Leu 25								
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ttt Phe	tcg Ser	aag Lys 35	gca Ala	cat His	cac His	gaa Glu	atg Met 40	aag Lys	aac Asn	cct Pro	gaa Glu	gcc Ala 45	tct Ser	aaa Lys	ttg Leu	144
aac Asn	aag Lys 50	agg Arg	tgc Cys	gct Ala	caa Gln	agc Ser 55	agt Ser	gaa Glu	tta Leu	tgt Cys	gat Asp 60	gcg Ala	ctg Leu	gac Asp	tca Ser	192
gac Asp 65	tgc Cys	tgc Cys	agt Ser	ggt Gly	gtt Val 70	tgc Cys	atg Met	gta Val	ttt Phe	ttc Phe 75	tgc Cys	cta Leu	taa	aact	gcc	241
gtga	atgt	ctt	ctct	atcc	cc t	С										263
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Phe	Ser	Lys 35	Ala	His	His	Glu	Met 40	Lys	Asn	Pro	Glu	Ala 45	Ser	Lys	Leu	
Asn	Lys 50	Arg	Cys	Ala	Gln	Ser 55	Ser	Glu	. Leu	. Cys	Asp 60	Ala	Leu	a Asp	Ser	
Asp 65	Cys	Cys	Ser	Gly	7 Val	. Cys	Met	. Val	Phe	Ph∈ 75	e Cys	Leu	l			
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                                                                       96
Trp Thr Phe Val Thr Ala Glu Asp Pro Arg Asp Gly Leu Arg Asn Leu
tta tcg aat gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Leu Ser Asn Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                                                                      192
aac gag agg tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt tat tca
Asn Glu Arg Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu Tyr Ser
gac tgc tgc agc tat tgc gtt ggt gct gtc tgc cta taaaactacc
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Asp Cys Cys Ser Tyr Cys Val Gly Ala Val Cys Leu
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                                                                          96
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Trp Thr Phe Ala Thr Ala Glu Asp Pro Arg Asn Gly Leu Glu Asn Leu
ttt tcg aag gca cat cac gaa atg aag aac cct gaa gac tct aaa ttg
                                                                         144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Asp Ser Lys Leu
                              40
gac aag agg tgc gtt aaa tat ctt gac cct tgt gac atg tta cgc cac
                                                                         192
Asp Lys Arg Cys Val Lys Tyr Leu Asp Pro Cys Asp Met Leu Arg His
acc tgc tgc ttt ggc ctg tgc gta cta ata gcc tgc atc taaaactgcc
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Thr Cys Cys Phe Gly Leu Cys Val Leu Ile Ala Cys Ile
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                                    10
tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg aat ctt
                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly Asn Leu
ttt tcg aat gca cat cac gaa atg aag aac ccc gaa gct tct aaa ttg
                                                                      144
Phe Ser Asn Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35
aac gag agg tgc ctt ggg ttt ggt gaa gtt tgc aat ttc ttt ttt cca
                                                                      192
Asn Glu Arg Cys Leu Gly Phe Gly Glu Val Cys Asn Phe Phe Pro
    50
                                                                      238
aac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta taaaactacc
Asn Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
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<223>
       13 may be Pro or hydroxy-Pro; Xaa at residue 18 may be Tyr, 125-I
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                                                                       96
Trp Thr Phe Ala Thr Ala Asp Asp Ser Ser Asn Gly Leu Glu Asn Leu
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ttt tcg aag gca cat cac gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                             40
        35
                                                                      192
aac aag agg tgc att cca caa ttt gat cct tgt gac atg gta cgt cac
Asn Lys Arg Cys Ile Pro Gln Phe Asp Pro Cys Asp Met Val Arg His
                                                                      240
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40

55

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35

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tgc agt ggg tgg tgc att gtt ctc gtc tgc gca Cys Ser Gly Trp Cys Ile Val Leu Val Cys Ala 20 25 30	
ctactcccct ctagtagtag taggcggccg ctctagagga	tccaagctta cgtacgcgtg 276
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163
Arg Cys Leu Glu Phe Gly Glu Val Cys Asn Phe Phe Pro Thr Cys
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gegeageetg aatggegaat gggaegegee etgtagegge geattaageg eggegggtgt
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ggtggttacg cgcagcgtga ccgctacact tgcagcgccc tagcgcccgc tcctttcgct
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       , 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phosph
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173

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<213>	Conu	s st:	riatı	ıs											
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Gly Xaa	a Xaa	Cys 20	Cys	Ser	Gly	Xaa	Cys 25	Phe	Leu	Xaa	Cys	Ala 30			
<212>	130 277 DNA Conu	s oma	aria												
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tgg aca															96
ctt tat Leu Ty															144
ttg aad Leu Asi 50															192
atg ata Met Ile 65	a aaa e Lys	att Ile	ggg Gly	ccg Pro 70	cct Pro	tgc Cys	tgc Cys	agt Ser	ggc Gly 75	tgg Trp	tgc Cys	ttt Phe	ttc Phe	gcc Ala 80	240
tgc gcc Cys Ala		aact	gcc (gtgat	tgtct	ct ct	tcct	ccct	c c						277
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Trp Thi	r Phe	Val 20	Thr	Ala	Val	Pro	His 25	Ser	Ser	Asn	Ala	Leu 30	Glu	Asn	
Leu Ty	r Leu 35	Lys	Ala	Arg	His	Glu 40	Met	Glu	Asn	Pro	Glu 45	Ala	Ser	Lys	

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Leu Asn Thr Arg Asp Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
Cys Ala
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<211> 30
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<213> Conus omaria
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<222>
      (1)..(30)
      Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
        6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
        be Trp or bromo-Trp
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Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
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Met Lys Leu Thr Cys Leu Met Ile Val Ala Val Leu Phe Leu Thr Ala
tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gca ttg gag aat
                                                                       96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
ctt tat ctg aag gca cgt cac gaa atq qaa aac ccc gaa gcc tct aaa
                                                                      144
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
ttg aac acg aga gac tac gat tgc gaa cct cct gga aat ttt tgt ggc
                                                                      192
Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
atg ata aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc
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Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
tgc gcc taaaactgcc gtgatgtctt ctcctccct c
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Cys Ala
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<212> PRT
<213> Conus aulicus
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Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
Leu Tyr Leu Lys Ala Arg His Glu Met Glu Asn Pro Glu Ala Ser Lys
Leu Asn Thr Arg Asp Tyr Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly
Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
Cys Ala
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<211> 30
<212> PRT
<213> Conus aulicus
<220>
<221>
      SITE
<222>
      (1)..(30)
      Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 5 may be Glu or
       gamma-carboxy-Glu; Xaa at residues 6, 7, 18 and 19 may be Pro or
       hydroxy-Pro; Xaa at residue 24 may be Trp or bromo-Trp
<400> 135
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Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
<210> 136
<211> 685
<212>
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<213> Conus marmoreus
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<221> CDS
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                                                                      60
caaactgtaa taaataatgc aagtetetet ttetgtttgt atetgacaga ttg aac
                                                                     116
                                                       Leu Asn
acg aga gac gat tgc gaa cct cct gga aat ttt tgt ggc atg ata
                                                                     164
Thr Arg Asp Asp Cys Glu Pro Pro Gly Asn Phe Cys Gly Met Ile
aaa att ggg ccg cct tgc tgc agt ggc tgg tgc ttt ttc gcc tgc gcc
                                                                     212
Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala Cys Ala
taaaactgcc gtgatgtctt ctcttcccct ctagtagtag taggcggccg ctctagagga
                                                                     272
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tccaagctta cgtacgcgtg catgcgacgt catagctctt ctatagtgtc acctaaattc
                                                                     332
aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa accctggcgt tacccaactt
                                                                     392
aatogoottg cagcacatoo cootttogoo agetggegta atagegaaqa ggecegcace
                                                                      452
gategeeett eecaacagtt gegeageetg aatggegaat gggaegegee etgtagegge
                                                                     512
gcattaagcg cggcgggtgt ggtggttacg ccgcagccgt gacccgctac acttgccagc
                                                                     572
goodtagege degeteettt egetttette etteetttet egecaegtte geeggetttt
                                                                     632
cccgtcaagc tctaaatcgg gggctccttt agggtccgat ttaagtgctt tac
                                                                     685
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<211>
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<213> Conus marmoreus
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Met Ile Lys Ile Gly Pro Pro Cys Cys Ser Gly Trp Cys Phe Phe Ala
Cys Ala
<210> 138
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       30
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      Conus marmoreus
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       (1)..(30)
       Xaa at residue 5 may be Glu or gamma-carboxy-Glu; Xaa at residues
        6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residue 24 may
        be Trp or bromo-Trp
<400> 138
Asp Asp Cys Xaa Xaa Xaa Gly Asn Phe Cys Gly Met Ile Lys Ile
Gly Xaa Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Ala Cys Ala
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       139
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       126
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      DNA
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       CDS
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      (1)..(96)
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Leu Asn Gln Arg Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Trp Pro
ata ctt gga cca ctg tgc tgc agt ggc tgg tgc tta tac gtc tgc atg
                                                                      96
Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
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taaaactgcc gtgatgtctt ctatcccctc
                                                                     126
<210> 140
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       32
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      PRT
<213> Conus regius
<400> 140
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Ile Leu Gly Pro Leu Cys Cys Ser Gly Trp Cys Leu Tyr Val Cys Met
                                25
<210>
      141
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       28
<212> PRT
<213> Conus regius
<220>
<221>
       SITE
<222>
      (1)..(28)
      Xaa at residues 11 and 22 may be Trp or bromo-Trp; Xaa at residue
       s 12 and 16 may be Pro or hydroxy-Pro; Xaa at residue 25 may be T
       yr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
       pho-Tyr
<400> 141
Asp Cys Leu Ser Lys Asn Ala Phe Cys Ala Xaa Xaa Ile Leu Gly Xaa
Leu Cys Cys Ser Gly Xaa Cys Leu Xaa Val Cys Met
            2.0
<210>
      142
<211>
      133
<212>
      DNA
<213>
      Conus radiatus
<220>
<221> CDS
<222> (2)..(103)
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a ttg aac aag aaa ggt gat gac tgc ctt gct gtt aaa aaa aat tgt ggc
                                                                      49
 Leu Asn Lys Lys Gly Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
ttt cca aaa ctt gga ggg cca tgc tgc agt ggc ttg tgc ttt ttc gtc
                                                                      97
Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
tgc gcc taaaactgcc gtgatgtctt ctcctccct
                                                                     133
Cys Ala
<210> 143
<211> 34
<212>
      PRT
<213>
      Conus radiatus
<400> 143
Leu Asn Lys Lys Gly Asp Cys Leu Ala Val Lys Lys Asn Cys Gly
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Phe Pro Lys Leu Gly Gly Pro Cys Cys Ser Gly Leu Cys Phe Phe Val
                                25
Cys Ala
<210> 144
<211> 30
<212> PRT
<213> Conus radiatus
<220>
<221> SITE
<222> (1)..(30)
<223> Xaa at residues 14 and 19 may be Pro or hydroxy-Pro.
<400> 144
Gly Asp Asp Cys Leu Ala Val Lys Lys Asn Cys Gly Phe Xaa Lys Leu
Gly Gly Xaa Cys Cys Ser Gly Leu Cys Phe Phe Val Cys Ala
<210> 145
<211> 127
<212> DNA
<213> Conus regius
<220>
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<222> (1)..(96)
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                                                                      48
Leu Asn Gln Ser Asp Cys Leu Pro Arg Asp Thr Phe Cys Ala Leu Pro
caa ctt gga cta ctg tgc tgc agt ggc cgg tgc tta ctc ttc tgc gtq
                                                                     96
Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
taaaactgcc gtgatgtctt ctcctcccct c
                                                                     127
<210> 146
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<213> Conus regius
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Gln Leu Gly Leu Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
<210> 147
<211> 28
<212> PRT
<213> Conus regius
<220>
<221> SITE
<222> (1)..(28)
<223> Xaa at residues 4 and 12 may be Pro or hydroxy-Pro.
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 Leu Cys Cys Ser Gly Arg Cys Leu Leu Phe Cys Val
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 <211>
       345
 <212> DNA
 <213> Conus aurisiacus
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                                                                       48
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tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
            20
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35
aac aag aga gat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat
                                                                      192
Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
    50
eca gga ete tge tge age gag att tge att gtt tgg tge aca
                                                                      234
Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
tgagtcgtat tctgctggta cattttgtgg cttcaacgga ggactctgct gcagcaacct
                                                                      294
ttgcttattt ttcgtgtgct taacatattc gtgatgtctt ctactcccat c
                                                                      345
<210> 149
<211>
      78
<212> PRT
<213> Conus aurisiacus
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Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
                        5.5
Pro Gly Leu Cys Cys Ser Glu Ile Cys Ile Val Trp Cys Thr
<210> 150
<211> 27
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<212> PRT
<213>
      Conus aurisiacus
<220>
<221>
      SITE
<222>
      Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 ma
       y be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or br
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Asp Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His Xaa Gly Leu
Cys Cys Ser Xaa Ile Cys Ile Val Xaa Cys Thr
<210> 151
<211> 412
<212> DNA
<213> Conus purpurascens
<220>
<221>
      CDS
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                                                                   48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat
                                                                   96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg
                                                                  144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
        35
                           40
gac aaa aag gaa gcc tgc tat gcg cct ggt act ttt tgt ggc ata aag
                                                                  192
Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys
ecc ggg cta tgc tgc agt gag ttt tgt etc ecg gge gtc tgc tte ggt
                                                                  240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
ggt taactgccgt gatgtcttct actcccctct gtgctacctg gcttgatctt
                                                                  293
Gly
tgatcggcgt gtgcccttca ctggttatga acccactgat cttacctctc ttgaaqqacc
                                                                  353
412
<210> 152
<211>
      81
<212> PRT
<213> Conus purpurascens
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 Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
 Asp Lys Lys Glu Ala Cys Tyr Ala Pro Gly Thr Phe Cys Gly Ile Lys 50 55 60
 Pro Gly Leu Cys Cys Ser Glu Phe Cys Leu Pro Gly Val Cys Phe Gly
 Gly
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<213>
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<221>
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       Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
       residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
       o or hydroxy-Pro
<400> 153
Xaa Ala Cys Xaa Ala Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
<210>
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<211>
       29
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<213> Conus purpurascens
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       (1)..(29)
       Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
<223>
       residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
       o or hydroxy-Pro
<400> 154
Xaa Ala Cys Xaa Ala Xaa Gly Thr Ala Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
<210>
      155
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       29
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       PRT
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       (1)..(29)
      Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
      residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
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lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr

<210> 158

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o or hydroxy-Pro
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Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
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       29
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        (1)..(29)
<223>
       Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
       residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 6, 14 and 24 may be Pr
       o or hydroxy-Pro
<400> 156
Xaa Ala Cys Xaa Ala Xaa Gly Ala Phe Cys Gly Ile Lys Xaa Gly Leu
                                     10
Cys Cys Ser Xaa Phe Cys Leu Xaa Gly Val Cys Phe Gly
<210>
       157
       289
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       DNA
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       CDS
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Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
                                     10
tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
            20
                                                     30
ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                            40
aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt
                                                                      192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt
                                                                      240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
gtt gat tct ggc taacagtgtg cgttggttag tgtcttctcc tcccctc
                                                                      289
Val Asp Ser Gly
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       Conus magus
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Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Thr
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
Val Asp Ser Gly
<210> 159
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<213> Conus magus
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<221>
       SITE
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       (1)..(32)
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       Xaa at residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
       hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
       Xaa at residue 25 may be Trp or bromo-Trp
<400> 159
Asp Gly Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Val Asp Ser
<210>
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      CDS
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tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
                                                                      96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg
                                                                     144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                            40
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aac aag aga gat gaa tgc tat cct cct ggt aca ttt tgt ggc atc aaa
                                                                      192
Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
                         55
cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca
                                                                      240
Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
                                        75
ttt gat ttt tgattgatgt cttctcctcc cctc
                                                                      273
Phe Asp Phe
<210> 161
<211> 83
<212> PRT
<213> Conus magus
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Asp Glu Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser
Phe Asp Phe
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       32
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      (1)..(32)
       Xaa at residue 2 may be Glu or gamma-carboxy-Glu; Xaa at residue
<223>
       4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
       or O-phospho-Tyr; Xaa at residues 5, 6and 14 may be Pro or hydro
       xy-Pro
<400> 162
Asp Xaa Cys Xaa Xaa Kaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
                                25
<210>
      163
<211>
      289
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      DNA
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<220>
<221> CDS
<222> (1)..(252)
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tgg Trp	aca Thr	ttc Phe	gtc Val 20	acg Thr	gct Ala	gat Asp	gac Asp	tcc Ser 25	aga Arg	tat Tyr	gga Gly	ctg Leu	aag Lys 30	gat Asp	ctg Leu	96
ttt Phe	ccg Pro	aag Lys 35	gaa Glu	cgt Arg	cat His	gaa Glu	atg Met 40	aag Lys	aac Asn	ccc Pro	gaa Glu	gcc Ala 45	tct Ser	aaa Lys	ttg Leu	144
aac Asn	cag Gln 50	aga Arg	gaa Glu	gcc Ala	tgc Cys	tat Tyr 55	aat Asn	gct Ala	ggt Gly	tca Ser	ttt Phe 60	tgt Cys	ggc Gly	atc Ile	cat His	192
cca Pro 65	gga Gly	ctc Leu	tgc Cys	tgc Cys	agc Ser 70	gag Glu	ttt Phe	tgc Cys	att Ile	ctt Leu 75	tgg Trp	tgc Cys	ata Ile	aca Thr	ttt Phe 80	240
gtt Val	gat Asp	tct Ser	ggc Gly	taac	ctgtg	gtg c	cgtto	ggtto	ga to	gtatt	ctcc	tcc	cato	:		289
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<400		164 Leu	ጥኮሎ	Cue	Val	Mo+	T 1 0	V-1	71.	17.0.7	T	Dl	.	m.	7 . 7	
1	цу	пеα	1111	5	val	mec	TTE	vai	10	va⊥	Leu	Pne	Leu	Thr 15	Ala	
Trp	Thr	Phe	Val 20	Thr	Ala	Asp	Asp	Ser 25	Arg	Tyr	Gly	Leu	Lys 30	Asp	Leu	
Phe	Pro	Lys 35	Glu	Arg	His	Glu	Met 40	Lys	Asn	Pro	Glu	Ala 45	Ser	Lys	Leu	
Asn	Gln 50	Arg	Glu	Ala		Tyr 55	Asn	Ala	Gly	Ser	Phe 60	Cys	Gly	Ile	His	
Pro 65	Gly	Leu	Cys	Cys	Ser 70	Glu	Phe	Cys		Leu 75	Trp	Cys	Ile		Phe 80	
Val	Asp	Ser	Gly													
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<400 Xaa 1		.65 Cys :	Xaa .	Asn . 5	Ala	Gly :	Ser	Phe	Cys (10	Gly :	Ile :	His :		Gly :	Leu	

Cys Cys Ser Xaa Phe Cys Ile Leu Xaa Cys Ile Thr Phe Val Asp Ser 20 25 30	
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ttt ccg aag gaa cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 35 40 45	144
aac cag aga gaa gcc tgc tat aat gct ggt aca ttt tgt ggc atc aaa Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys 50 55 60	192
cca gga ctt tgc tgc agc gcg ata tgc tta tcg ttt gtc tgc ata tca Pro Gly Leu Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser 65 70 75 80	240
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Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asp Leu 20 25 30	
Phe Pro Lys Glu Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu 35 40 45	
Asn Gln Arg Glu Ala Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Lys 50 60	
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       4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
        or O-phospho-Tyr; Xaa at residue 14 may be Pro or hydroxy-Pro
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Xaa Ala Cys Xaa Asn Ala Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Ala Ile Cys Leu Ser Phe Val Cys Ile Ser Phe Asp Phe
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tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg
                                                                      144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
                            40
gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag
                                                                      192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc gtc qqt
                                                                      240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
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ggt taactgccgt gatgtcttct cctcccctc
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Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
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Gly
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       Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
       residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may be
        Pro or hydroxy-Pro
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Xaa Ala Cys Xaa Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
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                                    10
tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg
                                                                      144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
                            40
gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag
                                                                      192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
ecc ggg cta tgc tgc agt gag ttg tgt tta ecg gec gtc tgc gtc ggt
                                                                      240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
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Gly
<210> 173
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Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
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       residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 14 and 24 may be Pro o
       r hydroxy-Pro
<400> 174
Xaa Ala Cys Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
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                                    10
tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
aac aag aga gaa ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cat
                                                                      192
Asn Lys Arg Glu Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile His
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cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt

240

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Ile Asp
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                             40
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Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
Ile Asp
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       p or bromo-Trp
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Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
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tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
                                                                      96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
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aac Asn	aag Lys 50	aga Arg	gat Asp	Gly	tgc Cys	tct Ser 55	agt Ser	ggt Gly	ggt Gly	aca Thr	ttt Phe 60	tgt Cys	ggc Gly	atc Ile	cat His	192
cca Pro 65	gga Gly	ctc Leu	tgc Cys	tgc Cys	agc Ser 70	gag Glu	ttt Phe	tgc Cys	ttt Phe	ctt Leu 75	tgg Trp	tgc Cys	ata Ile	aca Thr	ttt Phe 80	240
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<210 <211 <212 <213	.> ?>	179 82 PRT Conus	s stı	riatu	ıs											
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Trp	Thr	Phe	Val 20	Thr	Ala	Asp	Asp	Ser 25	Arg	Tyr	Gly	Leu	Lys 30	Asn	Leu	
Phe	Pro	Lys 35	Ala	Arg	His	Glu	Met 40	Lys	Asn	Pro	Glu	Ala 45	Ser	Lys	Leu	
Asn	Lys 50	Arg	Asp	Gly	Cys	Ser 55	Ser	Gly	Gly	Thr	Phe 60	Cys	Gly	Ile	His	
Pro 65	Gly	Leu	Cys	Cys	Ser 70	Glu	Phe	Cys	Phe	Leu 75	Trp	Cys	Ile	Thr	Phe 80	
Ile	Asp															
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<220 <221 <222 <223	> ; > > 2	SITE (1) Xaa a 14 m omo-T	t re	sidu e Pr	e 20 o or	may hyd	be roxy	Glu Pro	or g ; Xa	amma a at	-car res	boxy idue	-Glu 25	ı; Xa may	a at resi be Trp or	.due
<400 Asp 1		180 Cys	Ser	Ser 5	Gly	Gly	Thr	Phe	Cys 10	Gly	Ile	His	Xaa	Gly 15	Leu	
Cys	Cys	Ser	Xaa 20	Phe	Cys	Phe	Leu	Xaa 25	Cys	Ile	Thr		Ile 30	Asp		
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       Xaa at residues 6 and 14 may be Pro or hydroxy-Pro; Xaa at residu
       e 31may be Glu or gamma-carboxy-Glu
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Ser Lys Cys Phe Ser Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
Cys Cys Ser Val Arg Cys Phe Ser Leu Phe Cys Ile Ser Phe Xaa
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tgg aca ttc gtc acg gct gat gac tcc aga aat gga ctg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
                                                     30
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                            40
aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat
                                                                      192
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
                        55
cca gga ctc tgc tgc agc gag ctt tgc ctg gtt tgg tgc aca
                                                                      234
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Val Trp Cys Thr
tgagtgctat tcttctggta cattttgtgg cttcaacgga ggactctgct gcagcaacct
                                                                      294
ttgcttattt tcgtgtgctt aacatttcgt gatgtcttct ctattcccct c
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
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       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 14 may be Pro or
        hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
       Xaa at residue 25 may be Trp or bromo-Trp
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Cys Cys Ser Xaa Leu Cys Leu Val Xaa Cys Thr
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      CDS
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                                     10
tgg aca ttc gtc acg gct gat gac tcc aga tat gga ctg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
                                                     30
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
aac aag aga tat ggg tgc tct aat gct ggt gca ttt tgt ggc atc cat
                                                                      192
Asn Lys Arg Tyr Gly Cys Ser Asn Ala Gly Ala Phe Cys Gly Ile His
cca gga ctc tgc tgc agc gag ctt tgc ctg ggt tgg tgc aca
                                                                      234
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Gly Trp Cys Thr
tgagtgctat tctactggta cattttgtgg cttcaacgga ggactctgct gcagcaacct
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ttgcttattt tcgtgtgctt aacatttcgt gatgtcttct ctattcccct c
                                                                      345
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
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       hydroxy-Pro; Xaa at residue 20 may be Glu or gamma-carboxy-Glu;
       Xaa at residue 25 may be Trp or bromo-Trp
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Cys Cys Ser Xaa Leu Cys Leu Gly Xaa Cys Thr
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tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctc
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
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tet eeg aag gea eet eac gaa atg aag aac eee gaa gee tet aaa teg
                                                                      144
Ser Pro Lys Ala Pro His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
aac aag aga tat gag tgc tat cta ctg gta cat ttt tgt ggc atc aac
                                                                      192
Asn Lys Arg Tyr Glu Cys Tyr Leu Leu Val His Phe Cys Gly Ile Asn
gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca
                                                                      240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
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Phe Ser
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       Glu or gamma-carboxy-Glu
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Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
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atg ggt ctg tgc tgc agc gac aag tgc atg ctc gtc tgc ctg ccg
                                                                        93
Met Gly Leu Cys Cys Ser Asp Lys Cys Met Leu Val Cys Leu Pro
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tgatgtcttc tcctccctc
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       e 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
       yr or O-phospho-Tyr
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Cys Ser Asp Lys Cys Met Leu Val Cys Leu Xaa
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aat gtg ttt ctg tgc tgc agt ggc aac tgc ctt ctc atc tgc gtg ccg
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Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
                                25
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Asn Val Phe Leu Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Pro
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      Xaa at residues 5 and 28 may be Pro or hydroxy-Pro; Xaa at residu
       e 7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-T
       yr or O-phospho-Tyr
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Cys Cys Ser Gly Asn Cys Leu Leu Ile Cys Val Xaa
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tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat
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Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
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ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa
                                                                     144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
                            40
ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac
                                                                     192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
caa tgc tgc agt ggc tgg tgc att ttc gcc tgc ctc taaaactgtc
                                                                     238
Gln Cys Cys Ser Gly Trp Cys Ile Phe Ala Cys Leu
                    70
gtgatgtctt ctcctccct c
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Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
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Gly Xaa Cys Ile Phe Ala Cys Leu
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                                    10
tgg aca ttc gtc acg gct gtg cct cac tcc agc aat gcg ttg gag aat
                                                                       96
Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asn Ala Leu Glu Asn
            2.0
                                25
ctt tat ctg aag gca cat cat gaa atg aac aac ccc gag gac tct gaa
                                                                      144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
                            40
ttg aac aag agg tgc tat gat ggt ggg aca ggt tgt gac tct gga aac
                                                                      192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Gly Cys Asp Ser Gly Asn
caa tgc tgc agt ggc tgg tgc att ttc gtc tgc ctc taaaactgcc
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Gln Cys Cys Ser Gly Trp Cys Ile Phe Val Cys Leu
                    70
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                                                                      258
<210> 201
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       76
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<213> Conus dalli
<400> 201
Met Lys Leu Thr Cys Ile Met Ile Val Ala Val Leu Phe Leu Thr Ala
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	Leu	Tyr	Leu 35	Lys	Ala	His	His	Glu 40	Met	Asn	Asn	Pro	Glu 45	Asp	Ser	Glu		
	Leu	Asn 50	Lys	Arg	Cys	Tyr	Asp 55	Gly	Gly	Thr	Gly	Cys 60	Asp	Ser	Gly	Asn		
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			gtc Val														9	6
			ctg Leu 35														14	4
			aag Lys														19	2
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	gtga	atgt	ctt (ctcc	tece	ct c											25	9

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Leu Tyr Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Asn
Val Asp Lys Arg Cys Phe Glu Ser Trp Val Ala Cys Glu Ser Pro Lys
Arg Cys Cys Ser His Val Cys Leu Phe Val Cys Thr
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       205
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      24
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      PRT
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<220>
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       r hydroxy-Pro
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His Val Cys Leu Phe Val Cys Thr
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       253
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tgt caa ctc tct aca aat gcg agt tac gcc aga agt aag cag aag cat
                                                                          96
Cys Gln Leu Ser Thr Asn Ala Ser Tyr Ala Arg Ser Lys Gln Lys His
cgt gtt ctg agg tcg act gac aaa aac tcc aag ttg acc cag cgt tgc
                                                                         144
Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
aat gaa gct caa gaa cat tgc act caa aat cct gac tgc tgc agt gag
                                                                         192
Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
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50
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                                             60
tct tgc aat aag ttt gtc ggc aga tgc ttg tca gac tgatctgatg
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Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
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tcttctcctc ccatc
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<213> Conus distans
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Arg Val Leu Arg Ser Thr Asp Lys Asn Ser Lys Leu Thr Gln Arg Cys
Asn Glu Ala Gln Glu His Cys Thr Gln Asn Pro Asp Cys Cys Ser Glu
Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
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<211> 29
<212> PRT
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<220>
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<222>
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       Xaa at residues 3, 6 and 17 may be Glu or gamma-carboxy-Glu; Xaa
<223>
        at residue 12 may be Pro or hydroxy-Pro
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Xaa Ser Cys Asn Lys Phe Val Gly Arg Cys Leu Ser Asp
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tgg aca ttc gtc acg gct gtg cct gac tcc agc aat gcg ttg gag aat
                                                                      96
Trp Thr Phe Val Thr Ala Val Pro Asp Ser Ser Asn Ala Leu Glu Asn
                                25
                                                    30
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ctt tat ctg aag gca cat cat gaa atg aac aac ccc gaa gac tct gaa
                                                                     144
Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
                            40
ttg aac aag agg tgc tat gat ggt ggg aca agt tgt aac act gga aac
                                                                     192
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
                                            60
caa tgc tgc agt ggc tgg tgc att ttc ctc tgc ctc taaaactgcc
                                                                     238
Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
gtgatgtctt ctcttcccct c
                                                                     259
<210> 210
<211> 76
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Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Asp Ser Glu
Leu Asn Lys Arg Cys Tyr Asp Gly Gly Thr Ser Cys Asn Thr Gly Asn
Gln Cys Cys Ser Gly Trp Cys Ile Phe Leu Cys Leu
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<213> Conus ammiralis
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<221> SITE
<222>
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      Xaa at residue 2 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Ty
       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 18 may be Trp or
       bromo-Trp
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Gly Xaa Cys Ile Phe Leu Cys Leu
            20
<210> 212
<211> 286
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<213> Conus textile
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<222> (25)..(255)
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tcc agc aat gcg ttg gag aat ctt tat ctg aag gca cat cat gaa atg Ser Ser Asn Ala Leu Glu Asn Leu Tyr Leu Lys Ala His His Glu Met 30 35 40	147												
aac aac ccc gaa gcc tct gaa ttg aac aag agg tgc tat gat agt ggg Asn Asn Pro Glu Ala Ser Glu Leu Asn Lys Arg Cys Tyr Asp Ser Gly 45 50 55	195												
aca agt tgt aac act gga aac caa tgc tgc agt ggc tgg tgc att ttc Thr Ser Cys Asn Thr Gly Asn Gln Cys Cys Ser Gly Trp Cys Ile Phe 60 65 70	243												
gtc tct tgc ctc taaaactacc gtgatgtctt ctcctcccct c Val Ser Cys Leu 75	286												
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Leu Tyr Leu Lys Ala His His Glu Met Asn Asn Pro Glu Ala Ser Glu 35 40 45													
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Gly Xaa Cys Ile Phe Val Ser Cys Leu 20 25													

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<212>
       DNA
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tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt
                                                                       96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
ttt tcg aaa tca cgt gac gaa atg gag gac ccc gaa gct tct aaa ttg
                                                                      144
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
gag aaa agg gat tgc caa gca cta tgg gat tat tgt cca gta ccg ctc
                                                                      192
Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
                        55
ttg tca tcg ggt gat tgc tgc tat ggc tta atc tgt ggc cct ttc qtc
                                                                      240
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                                                                      272
Cys Ile Gly Trp
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<213>
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Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
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Glu Lys Arg Asp Cys Gln Ala Leu Trp Asp Tyr Cys Pro Val Pro Leu
Leu Ser Ser Gly Asp Cys Cys Tyr Gly Leu Ile Cys Gly Pro Phe Val
Cys Ile Gly Trp
<210> 217
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       33
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<213> Conus gloriamaris
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<222> (1)..(33)
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        8 and 21 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr; Xaa at residues 10, 12 and 27 may be P
       ro or hydroxy-Pro
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Gly Asp Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Ile Gly
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                                                                       96
Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
ttc tcg aaa tca cgt gac gaa atg gag gat acc gat cct tct aaa ttg
                                                                      144
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
                            40
gag aac aga aaa act tgc caa aga agg tgg gat ttt tgt cca gga tcg
                                                                      192
Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
                        55
                                            60
ctc gtt gga gtg ata act tgc tgc ggt ggc tta atc tgt ttt ctg ttc
                                                                      240
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Phe Cys Val
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<211> 83
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<213> Conus omaria
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Trp Thr Phe Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
Phe Ser Lys Ser Arg Asp Glu Met Glu Asp Thr Asp Pro Ser Lys Leu
Glu Asn Arg Lys Thr Cys Gln Arg Arg Trp Asp Phe Cys Pro Gly Ser
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Phe Cys Val
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       e Pro or hydroxy-Pro
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Val Ile Thr Cys Cys Gly Gly Leu Ile Cys Phe Leu Phe Phe Cys Val
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                                    10
tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat ctt
                                                                       96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn Leu
ttt tcg aaa tta cgt gac gaa atg gag gac ccc gaa ggt tct aaa ttg
                                                                      144
Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
gag aaa aag gat tgc caa gaa aaa tgg gat tat tgt cca gta ccg ttc
                                                                      192
Glu Lys Lys Asp Cys Gln Glu Lys Trp Asp Tyr Cys Pro Val Pro Phe
ttg gga tcg agg tat tgc tgc gat ggc ttt atc tgt cca tct ttc ttc
                                                                      240
Leu Gly Ser Arg Tyr Cys Cys Asp Gly Phe Ile Cys Pro Ser Phe Phe
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Cys Ala
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<211> 82
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Phe Ser Lys Leu Arg Asp Glu Met Glu Asp Pro Glu Gly Ser Lys Leu
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Cys Ala
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        6 may be Trp or bromo-Trp; Xaa at residues 8 and 18 may be Tyr, 1
       25-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
       yr; Xaa at residues 10, 12 and 26 may be Pro or hydroxy-Pro
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Arg Xaa Cys Cys Asp Gly Phe Ile Cys Xaa Ser Phe Phe Cys Ala
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                                      10
tgg acg cta gtc atg gct gat gac tcc aac aat gga ctg gcg aat cat
                                                                          96
Trp Thr Leu Val Met Ala Asp Asp Ser Asn Asn Gly Leu Ala Asn His
                                  25
                                                       30
ttt tgg aaa tca cgt gac gaa atg gag gac cct gaa gct tct aaa ttg
                                                                         144
Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
gag aaa agg gat tgc caa ggc gaa tgg gag ttt tgt ata gta ccg gtc
                                                                         192
Glu Lys Arg Asp Cys Gln Gly Glu Trp Glu Phe Cys Ile Val Pro Val
ctt gga ttt gtg tat tgc tgc ccc tgg ctt atc tgt ggc cct ttc gtc
                                                                         240
Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
                                          75
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Cys Val Asp Ile
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<213> Conus dalli
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Phe Trp Lys Ser Arg Asp Glu Met Glu Asp Pro Glu Ala Ser Lys Leu
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Leu Gly Phe Val Tyr Cys Cys Pro Trp Leu Ile Cys Gly Pro Phe Val
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       Xaa at residues 5 and 7 may be Glu or gamma-carboxy-Glu; Xaa at r
<223>
       esidues 6 and 22 may be Trp or bromo-Trp; Xaa at residues 12, 21
       and 27 may be Pro or hydroxy-Pro;
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       SITE
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       (1)..(33)
       Xaa at residue 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-T
       yr, O-sulpho-Tyr or O-phospho-Tyr
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Ile
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                                     10
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                                                                       96
Trp Thr Phe Val Met Ala Asp Asp Pro Arg Asp Glu Pro Glu Ala Arg
             20
                                 25
gac gaa atg aac ccc gca gcc tct aaa ttg aac gag aga ggc tgc ctt
                                                                      144
Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
                             40
gaa gtt gat tat ttt tgc ggc ata ccg ttt gtg aac aac ggg cta tgc
                                                                      192
Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
tgc agt ggc aat tgt gtt ttt gtc tgc aca ccc caa ggg aag
                                                                      234
Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
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Asp Glu Met Asn Pro Ala Ala Ser Lys Leu Asn Glu Arg Gly Cys Leu
                            40
Glu Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys
Cys Ser Gly Asn Cys Val Phe Val Cys Thr Pro Gln Gly Lys
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       (1)..(31)
      Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residue
<223>
       7 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
       or O-phospho-Tyr; Xaa at residues 12 and 30 may be Pro or hydrox
       y-Pro
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Gly Cys Leu Xaa Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
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<211> 428
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attcac	tgcc	aaac	ctgto	cat a	aaata	atttç	ga gt	ctct	cttt	: ctg	rtttt	tat	ctga	ıcaga	tt	120
g aac Asn 1	gag a Glu A	ga g rg F	gac t Asp (igc (Cys I	ctt a Leu <i>P</i>	at q Asn V	gtt g /al A	sp 1	at t 'yr E .0	tt t he C	gc g	ggc a Sly I	le F	cg t ro P	tt he	169
gtg aa Val As	c aac n Asn	ggg Gly 20	cta Leu	ı tgo ı Cys	tgc Cys	agt Sei	ggc Gly 25	aat Asn	tgt Cys	gtt Val	ttt Phe	gto Val	tgc Cys	aca Thr		217
ccc ca Pro Gl:	a ggg n Gly 35	aag Lys	ta <i>a</i>	aact	gcc	gtga	tgtc	tt c	tctt	cccc	t ct	agta	gtag	-		269
taggcg	gccg	ctct	agag	ıga t	.ccaa	gatt	a cg	tacg	cgtg	cat	gcga	.cgt	cata	gctc	tt	329
ctatag	tgtc	acct	aaat	tc a	attc	actg	id cc	gtcc	gttt	tac	aacg	tcg	tgac	tggg	aa	389
aaccct	ggcg	ttac	ccaa	.ct t	aatc	gcct	t gc	agca	cat							428
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<400> Asn Glu 1	231 ı Arg	Asp	Cys 5	Leu	Asn	Val	Asp	Tyr 10	Phe	Cys	Gly	Ile	Pro 15	Phe		
Val Asr	n Asn	Gly 20	Leu	Cys	Cys	Ser	Gly 25	Asn	Cys	Val	Phe	Val 30	Cys	Thr		
Pro Glr	Gly 35	Lys														
<210> <211> <212> <213>	232 30 PRT Conus	s ma:	rmor	eus												
<220> <221> <222> <223>	SITE (1) Xaa a r, O- e Pro	at re sulp	esid pho-	ryr	or O-	be ! -pho:	Tyr, spho-	125- Tyr,	-I-Ty : Xaa	yr, m a at	nono- res:	-iodo idues	o-Tyı s 11	c, di and	-iodo 29 ma	o-Ty ay b
<400> Cys Leu 1	232 Asn	Val	Asp 5	Xaa	Phe	Cys	Gly	Ile 10	Xaa	Phe	Val	Asn	Asn 15	Gly		
Leu Cys	Cys	Ser 20	Gly	Asn	Cys	Val	Phe	Val	Cys	Thr	Xaa	Gln				

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                                                                       116
                                                  Leu Asp Lys Arg
 gag tgc ctg gaa gct gat tat tat tgc gtc tta ccg ttt gtg ggc aac
                                                                       164
 Glu Cys Leu Glu Ala Asp Tyr Tyr Cys Val Leu Pro Phe Val Gly Asn
                     10
                                                              20
 ggg atg tgc tgc agt ggc att tgt gtt ttt gtc tgc ata gcc caa cgc
                                                                       212
 Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
                 25
 ttt aaa acc gtc tga
                                                                       227
Phe Lys Thr Val
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       PRT
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       Conus marmoreus
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Phe Val Gly Asn Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys
Ile Ala Gln Arg Phe Lys Thr Val
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       esidues 7 and 8 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr
       , O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 12 may be Pro or
       hydroxy-Pro
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Xaa Cys Leu Xaa Ala Asp Xaa Xaa Cys Val Leu Xaa Phe Val Gly Asn
Gly Met Cys Cys Ser Gly Ile Cys Val Phe Val Cys Ile Ala Gln Arg
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Phe Lys Thr Val
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                                                                        120
atctgacaga ttg aac gag aga gac tgc ctt gaa cct gat tat gtt tgc
                                                                        169
            Leu Asn Glu Arg Asp Cys Leu Glu Pro Asp Tyr Val Cys
ggc ata ccg ttt gtg ttc aac ggg cta tgc tgc agt gga att tgt gtt
                                                                        217
Gly Ile Pro Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val
    15
                         20
ttt atc tgc ata gcc caa aag tat taaaacgccg tgatgtcttc tattcccatc
                                                                       271
Phe Ile Cys Ile Ala Gln Lys Tyr
                     35
tagtagtagt aggeggeege tetagaggat ecaagettae gtaegegtge atgegaegte
                                                                       331
atagetette tatagtgtea cetaaattea atteaetgge egtegtttta caaegtegtg
                                                                       391
actgggaaaa ccctggcgtt acccaactta atcgccttgc agcacatccc cctttcgcca
                                                                       451
gctggcgtaa tagccgaaga ggcccgcacc gatcgccctt cccaacagtt gcgcagcctg
                                                                       511
aatggcgaat gggg
                                                                       525
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      Conus marmoreus
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Phe Val Phe Asn Gly Leu Cys Cys Ser Gly Ile Cys Val Phe Ile Cys
Ile Ala Gln Lys Tyr
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       SITE
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       (1)..(33)
      Xaa at residue 4 may be Glu or gamma-carboxy-Glu; Xaa at residues
<223>
        5 and 12 may be Pro or hydroxy-Pro; Xaa at residues 7 and 33 may
       be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
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-phospho-Tyr

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Xaa
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atotgtocat ocatotatto attoattogo tgtoaaactg taatacatat tagaatotot 12
ctttctgttt gtatctgaca gattg gag aaa agg gcg tgc agc aaa aaa tgg 17: Glu Lys Arg Ala Cys Ser Lys Lys Trp 1 5
gaa tat tgt ata gta ccg atc ctt gga ttc gta tat tgc tgc cct ggc Glu Tyr Cys Ile Val Pro Ile Leu Gly Phe Val Tyr Cys Cys Pro Gly 10 20 25
tta atc tgt ggt cct ttc gtc tgc gtt tgatagtgat gtcttctcct Leu Ile Cys Gly Pro Phe Val Cys Val 30
cccatctagt agtagtaggc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 32
gacgtcatag ctcttctata gtgtcaccta aattcaattc
gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catcccctt 44
tegecagetg gegtaataag egaagaggee egeacegate geeetteeca acagttgege 50°
agcctgaatg gcgaaatggg acgcgcctg 53
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Leu Gly Phe Val Tyr Cys Cys Pro Gly Leu Ile Cys Gly Pro Phe Val 20 25 30
Cys Val
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<213> Conus marmoreus
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Val Xaa Cys Cys Xaa Gly Leu Ile Cys Gly Xaa Phe Val Cys Val 20 25 30
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gtctctcttt ctgtttttat ctgacaga ttg aac gag aga gac tgc ctt aat 172 Leu Asn Glu Arg Asp Cys Leu Asn 1 5
gtt gat tat ttt tgt ggc ata ccg ttt gtg aac aac ggg cta tgc tgc Val Asp Tyr Phe Cys Gly Ile Pro Phe Val Asn Asn Gly Leu Cys Cys 10 15 20
agt ggc aat tgt gtt ttt tgt ctg cac acc cca agg gaa gta aaa ctg Ser Gly Asn Cys Val Phe Cys Leu His Thr Pro Arg Glu Val Lys Leu 25 30 35 40
ccg tgatgtcttc tcttcccctc tagtagtagt aggcggccgc tctagaggat 321 Pro
ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca cctaaattca 381
attcactggc cgtcgtttta caacgtcgtg actgggaaaa ccctggcgtt acccaactta 441
ategeettge ageacatece cetttegeea getggegtaa tagegaagag geeegeaceg 501
ategecette ecaacagttg egeageetga atggegaatg ggaegegeee t 552
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        ay be Pro or hydroxy-Pro; Xaa at residue 33 may be Glu or gamma-c
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 Asp Cys Leu Asn Val Asp Xaa Phe Cys Gly Ile Xaa Phe Val Asn Asn
 Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Cys Leu His Thr Xaa Arg
Xaa Val Lys Leu Xaa
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                                                                      112
                             Arg Ser Lys Arg Cys Leu Val Tyr Gly
aca cct tgt gac tgg ctg acc att gcg ggt atg gag tgc tgc agt aaa
                                                                      160
Thr Pro Cys Asp Trp Leu Thr Ile Ala Gly Met Glu Cys Cys Ser Lys
aag tgc ttt atg atg tgc tgg taaaactgcc gtgatgtctt ctactcccct c
                                                                      212
Lys Cys Phe Met Met Cys Trp
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      32
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Ile Ala Gly Met Glu Cys Cys Ser Lys Lys Cys Phe Met Met Cys Trp
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        r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 7 may be Pro or
        hydroxy-Pro; Xaa at residues 10 and 28 may be Trp or bromo-Trp; X
        aa at residue 17 may be Glu or gamma-carboxy-Glu
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 Cys Leu Val Xaa Gly Thr Xaa Cys Asp Xaa Leu Thr Ile Ala Gly Met
Xaa Cys Cys Ser Lys Lys Cys Phe Met Met Cys Xaa
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tta ata aag aac ggg cta tgc tgc agt cag att tgt tta ggt gtc tgc
                                                                       97
Leu Ile Lys Asn Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys
                                 25
gca aaa gtg ttt taaaactgcc gtgatgtctt ctactcccat
                                                                      139
Ala Lys Val Phe
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       36
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<213> Conus radiatus
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        esidue 12 may be Pro or hydroxy-Pro
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 Gly Leu Cys Cys Ser Gln Ile Cys Leu Gly Val Cys Ala Lys Val Phe
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 gto ttt gga ago tao ota tgo tgo agt ggo ogg tgt gta tto gto tgo
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 Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
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Ile
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Val Phe Gly Ser Tyr Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys
Ile
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       esidue 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-su
       lpho-Tyr or O-phospho-Tyr
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Xaa Leu Cys Cys Ser Gly Arg Cys Val Phe Val Cys Ile
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 gtc ttt gca agc ttc cta tgc tgc agt ggc ctg tgt gta ttc gtc tgc
                                                                       97
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Phe Leu Cys Cys Ser Gly Leu Cys Val Phe Val Cys Ile
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       Xaa at residue 4 may be Pro or hydroxy-Pro; Xaa at residue 17 may
        be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O
       -phospho-Tyr
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Xaa Leu Cys Cys Ser Gly Arg Cys Ile Phe Val Cys Val
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ata att gga gcg ttt ctg tgc tgt agt ggc tac tgc ctt gtc gtc tgc
                                                                       96
Ile Ile Gly Ala Phe Leu Cys Cys Ser Gly Tyr Cys Leu Val Val Cys
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       o-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
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tgt cag ttc atc gta gct ggc gac tcg agt gat ggc cag gag aat cct
                                                                      96
Cys Gln Phe Ile Val Ala Gly Asp Ser Ser Asp Gly Gln Glu Asn Pro
            20
gct ctg agg tca cct agc gat tcc tct ggg aaa atg tca tca atg aag
                                                                     144
Ala Leu Arg Ser Pro Ser Asp Ser Ser Gly Lys Met Ser Ser Met Lys
        35
cgc ttc cag aca cgg ctg atg gtg ggg caa tct gca tcg aaa aga cca
                                                                     192
Arg Phe Gln Thr Arg Leu Met Val Gly Gln Ser Ala Ser Lys Arg Pro
age aag agg gae tge ate eee gge gge gaa aat tgt gat gta tte ega
                                                                     240
Ser Lys Arg Asp Cys Ile Pro Gly Gly Glu Asn Cys Asp Val Phe Arg
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cca tac cgg tgc tgc agt gga tat tgc ata cta ctc ctt tgc gca
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319

90

85

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CDS

(147)..(233)

misc_feature

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ctt tgt ttc cgc tcg gat cac ata gga tgc tgc agt ggc aag tgc gca Leu Cys Phe Arg Ser Asp His Ile Gly Cys Cys Ser Gly Lys Cys Ala 10 15 20 25	221
ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcctcccat ctagtagtag Phe Val Cys Leu	273
taggcggccg ctctagagga tccaagctta cgtacgcgtg catgcgacgt catagctctt	333
ctatagtgtc acctaaattc aattcactgg ccgtcgtttt acaacgtcgt gactgggaaa	393
accetggegt tacceaactt aategeettg cageacatee ceetttegee agetggegta	453
atagegaaga ggeeegeace gategeeett eccaacagtt tgegeageet gaatggegaa	513
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aagggttncc gaattantgc tttaccggna cccttgaccc ccaaaaaaac ttggantaag	753
gggngatggn tenegtaant gggggeeate neecetgaan agaacggttt tteneceett	813
ttgacngttg ggngttccnc ggtttttaaa aaangggacc ttttntttcc aaaactggga	873
ananacctaa accctatttt tggggctatt tttttgantt tnaaanggga ttttgcccca	933
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Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
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Ile Gln Cys Cys Ser Gly Lys Cys Ala Phe Val Cys Leu
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                                                                     112
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Glu Val Cys Arg Arg Tyr Glu Phe Val Gly Cys Cys Ser Gly Lys Cys
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       Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
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Val Gly Cys Cys Ser Gly Lys Cys Phe Phe Val Cys Ser
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                                                                      99
Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile
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Leu Lys Ser Cys Val Ser
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ttg acc gcc tgg aca ttc gtc acg gct gtg cct cac tcc agc gat gta
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Leu Thr Ala Trp Thr Phe Val Thr Ala Val Pro His Ser Ser Asp Val
    15
                         20
ttg gag aat ctt tat ctg aag gca ctt cac gaa acg gaa aac cac gaa
                                                                       207
Leu Glu Asn Leu Tyr Leu Lys Ala Leu His Glu Thr Glu Asn His Glu
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Phe Leu Trp Cys Ala
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Cys Ala
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       sidues 6, 7, 18 and 19 may be Pro or hydroxy-Pro; Xaa at residues
        24 and 28 may be Trp or bromo-Trp
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His His Glu Met Asn Asn Pro Glu Asp Ser Glu Leu Asn Lys Arg Cys
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ctgtgctacc tacctggctt gatctttgat tggcgcgtgc ccttcactgg ttatgaaccc 2													
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tgg Trp 35	ggg Gly	cag Gln	gca Ala	gga Gly	gga Gly 40	tgg Trp	Gly	aaa Lys	ctt Leu	ttt Phe 45	ccg Pro	atg Met	gca Ala	cgc Arg	gac Asp 50	201
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Gly (Gly	Trp 35	Gly	Gln	Ala	Gly	Gly 40	Trp	Gly	Lys	Leu	Phe 45	Pro	Met	Ala	
Arg 1	Asp 50	Glu i	Met	Lys	Asn	Ser 55	Glu	Val	Ser	Lys	Leu 60	Asp	Asn	Lys	Arg	
Lys (65	Cys .	Ala	Ala .	Ala	Gly 70	Glu .	Ala	Cys	Val	Ile 75	Pro	Ile	Ile	Gly	Asn 80	
Val 1	Phe (Cys (Cys :	Lys 35	Gly	Tyr	Cys	Leu	Phe 90	Val	Cys	Ile	Ser			
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Phe Arg Lys Ala Arg Asp Asn Met Lys Asn Ala Lys Ala Ser Thr Leu
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Phe Phe Leu Asp Glu Glu Cys Cys Thr Gly Ser Cys His Val Phe Cys
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Val Leu
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Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Glu Asn Leu
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                                                                      144
Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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                                                                      192
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acc o Thr 1 15	gcc Ala	tcg Ser	gct Ala	Asp	gac Asp 20	tcc Ser	aga Arg	aat Asn	gga Gly	ttc Phe 25	gag Glu	aat Asn .	cga Arg	Asn	gga Gly 30	96
gaa (Glu <i>l</i>	cga Arg	aac Asn	GIU A	aac Asn 35	gaa Glu	atg : Met :	aag Lys	Asn	ctc Leu 40	gaa Glu .	gcc Ala	tct : Ser :	Lys	ttg Leu 45	aac Asn	144
agg a Arg <i>l</i>	aga Arg	ASP	ggc (Gly <i>1</i> 50	gat Asp	tgc Cys	gtt d Val 2	4sp	ggt Gly 55	ggt Gly	gaa Glu	ttt Phe	Cys (ggc Gly 60	ttt (Phe	ccg Pro	192
aaa a Lys]	att [le	gga Gly 65	Gly 1	cca Pro (tgc · Cys ·	Cys S	agt (Ser (ggc Gly	tgg Trp	tgc : Cys :	Phe :	ttc q Phe V 75	gtc : /al (tgc (Cys)	tta Leu	240

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        or bromo-Trp
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agt ggt gta gtt tgt ggc ttt ccg aaa cct gaa cca cac tgc tgc agt Ser Gly Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser 50 55 60	2
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Arg Asn Glu Asn Glu Met Arg Asp Arg Arg Asp Cys Gln Asp Ser Gly 35 40	
Val Val Cys Gly Phe Pro Lys Pro Glu Pro His Cys Cys Ser Gly Trp 50 55	
Cys Leu Phe Val Cys Ala 65 70	
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His Cys Cys Ser Gly Xaa Cys Leu Phe Val Cys Ala 20 25	
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48

96

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Thr Ala Trp Thr Phe Val Thr Ala Asp Ser Ile Arg Ala Leu Glu Asp
 ttt ttt gcg aag gca cgt gac gaa atg gaa aac agc gga gct tct cca
                                                                      144
Phe Phe Āla Lys Āla Arg Āsp Glu Met Glu Asn Ser Gly Āla Ser Pro
ttg aac gag aga gac tgc cga cct gta ggt caa tat tgt ggc ata ccg
                                                                      192
Leu Asn Glu Arg Asp Cys Arg Pro Val Gly Gln Tyr Cys Gly Ile Pro
tat aag cac aac tgg cga tgc tgc agt cag ctt tgt gca att atc tgt
                                                                      240
Tyr Lys His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys
gtt tcc taacccctct gatcctactc tctgaagacc tccgggattc aacatccaaa
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Val Ser
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Ala Lys Ala Arg Asp Glu Met Glu Asn Ser Gly Ala Ser Pro Leu Asn
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His Asn Trp Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
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        es 8 and 13 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
        sulpho-Tyr or O-phospho-Tyr; Xaa at residue 17 may be Trp or brom
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 Asp Cys Arg Xaa Val Gly Gln Xaa Cys Gly Ile Xaa Xaa Lys His Asn
 Xaa Arg Cys Cys Ser Gln Leu Cys Ala Ile Ile Cys Val Ser
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acc gcc tgg aca ttc gtc aag gct gat gac tcc ata aat gga ttg gag
                                                                          96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Ile Asn Gly Leu Glu
aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct
                                                                         144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
                                      40
aaa ttg aac gag agg tgc ctt gaa aag ggt gta ctt tgt gat ccg agt
                                                                         192
Lys Leu Asn Glu Arg Cys Leu Glu Lys Gly Val Leu Cys Asp Pro Ser
get gga aac tge tgt agt gge gaa tge gtt tta gte tge etc
                                                                         234
Ala Gly Asn Cys Cys Ser Gly Glu Cys Val Leu Val Cys Leu
                             70
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acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gaa ttg gag
                                                                       96
Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Glu Leu Glu
                    2.0
aat ctt ttt ctg aag gca tat cac gaa atg aac tcc gaa gcc tct aaa
                                                                      144
Asn Leu Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys
ttg gac aag aaa gag tgc gtt gct ggt agt cac ttt tgt ggt ttt ccg
                                                                      192
Leu Asp Lys Lys Glu Cys Val Ala Gly Ser His Phe Cys Gly Phe Pro
aaa att gga ggg cca tgc tgc agt ggc tgg tgc ttt ttc gtc tgc ttg
                                                                      240
Lys Ile Gly Gly Pro Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Leu
                            70
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Phe Leu Lys Ala Tyr His Glu Met Asn Ser Glu Ala Ser Lys Leu Asp
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       12 and 17 may be Pro or hydroxy-Pro; Xaa at residue 22 may be Tr
       p or bromo-Trp
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Xaa Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Leu
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acc gcc tgg aca ttc atc acg gct gat gac tcc ata aat gga ctg gag
                                                                       96
Thr Ala Trp Thr Phe Ile Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu
                    20
                                                             30
gat aga ggc ata tgg ggg gaa cct ttg tcg aag gca cgt gac gaa atg
                                                                      144
Asp Arg Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met
aac ccc gaa gtc tct aaa cgg gat tgc tgg cct caa tat tgg ttt tgt
                                                                      192
Asn Pro Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys
                                55
ggc cta cag agg gga tgc tgc cca ggg act act tgc ttc ttc ctt tgc
                                                                      240
Gly Leu Gln Arg Gly Cys Cys Pro Gly Thr Thr Cys Phe Phe Leu Cys
                            70
ttt tagtgatctc ttcgactccc ttctgtgcta cctggcttga cctttgattg
                                                                      293
Phe
gegegtgeee tteactggtt ataaaceeet etgtteetee tetetggaeg etteggggtg
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tecageatee aaataaageg aegteeecaa aaaaaaaaa aaaaaaa
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Gly Ile Trp Gly Glu Pro Leu Ser Lys Ala Arg Asp Glu Met Asn Pro
Glu Val Ser Lys Arg Asp Cys Trp Pro Gln Tyr Trp Phe Cys Gly Leu
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<223>
       4 and 17 may be Pro or hydroxy-Pro; Xaa at residue 6 may be Tyr,
       125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho
       -Tyr
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Xaa Gly Thr Thr Cys Phe Phe Leu Cys Phe
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aac gcc tgg aca ttc gcc acg gct gtt gac tcc aaa cat gca ctg gcg
                                                                       96
Asn Ala Trp Thr Phe Ala Thr Ala Val Asp Ser Lys His Ala Leu Ala
                    20
aaa ctt ttt atg aag gca cgt gac gaa atg tat aac ccc gat gcc act
                                                                      144
Lys Leu Phe Met Lys Ala Arg Asp Glu Met Tyr Asn Pro Asp Ala Thr
                                    40
aaa ttg gac gat aag aga tgg tgc gct tta gat ggt gaa ctt tgt atc
                                                                      192
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Lys Leu Asp Asp Lys Arg Trp Cys Ala Leu Asp Gly Glu Leu Cys Ile

		50					55					60			
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tac to Tyr Cy 80	s Val	tag	ttga	act ·	gccg.	tgat	gt c	ttct	actc	c cci	tctg	tgct			289
acccct	ggtt	tgat	cttt	ga t	tgcc	ctgt	g cc	cttca	actg	atta	atga	atc	cctct	tgatcc	349
tactct	ctga	agac	ctct	tg g	ggtc	caac	a tc	caaat	caaa	gcga	acat	ccc .	aaaa	aaaaaa	409
aaaaaa	ıaaaa														419
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Phe Me	t Lys 35	Ala	Arg	Asp	Glu	Met 40	Tyr	Asn	Pro	Asp	Ala 45	Thr	Lys	Leu	
Asp As 50	p Lys	Arg	Trp	Cys	Ala 55	Leu	Asp	Gly	Glu	Leu 60	Cys	Ile	Ile	Pro	
Val Il 65	e Gly	Ser	Ile	Phe 70	Cys	Cys	His	Gly	Ile 75	Cys	Met	Ile	Tyr	Cys 80	
Val															
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acc gcc tcg gta ttc atc acg gct gat gac tcc aga aat gga atc gag
                                                                       96
 Thr Ala Ser Val Phe Ile Thr Ala Asp Asp Ser Arg Asn Gly Ile Glu
aat ctt cct cgg atg aga cgt cac gaa atg aag aac ccc aaa gcc tct
                                                                      144
Asn Leu Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser
                                     40
aag ttg aac aag aga cag tgc cgt gta gaa ggt gaa att tgt ggc atg
                                                                      192
Lys Leu Asn Lys Arg Gln Cys Arg Val Glu Gly Glu Ile Cys Gly Met
ctg ttt gaa gca caa tgc tgc gat ggc tgg tgc ttt ttc gtc tgc atg
                                                                      240
Leu Phe Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
taaaactgcc gtgatgtctt ctactctcct ctgtgctacc tgccctgatc tttgattggc
                                                                      300
tegegeeett cattggttat gaaceeetet gateetacte tetggaggee teaggggtee
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agcatctaaa taaagcgaca tcacaatcaa aaaaaaaaa aaaaaaaa
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Pro Arg Met Arg Arg His Glu Met Lys Asn Pro Lys Ala Ser Lys Leu
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Glu Ala Gln Cys Cys Asp Gly Trp Cys Phe Phe Val Cys Met
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        or bromo-Trp
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acc gcc tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag
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Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu
aat ctt ttt ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct
                                                                      144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
                35
aaa ttg aac aag agg tgc gtt gac cct ggt gaa ttt tgt ggt ccg gga
                                                                      192
Lys Leu Asn Lys Arg Cys Val Asp Pro Gly Glu Phe Cys Gly Pro Gly
ttt gga gat tgc tgc act ggc ttc tgc ctt tta gtc tgc atc
                                                                      234
Phe Gly Asp Cys Cys Thr Gly Phe Cys Leu Leu Val Cys Ile
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                                                                      281
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Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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       e 6 may be Glu or gamma-carboxy-Glu
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acc gcc tgg aca ttc gtc atg gct gat gac tcc aga aat gat ttg gag
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Thr Ala Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu
                    20
aat ctt ttt ctg aag gca cgt cat gaa atg aag aac ccc gaa gct tct
                                                                      144
Asn Leu Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser
                35
aaa ttg aac aag aga tgc ctt cca aat ggt gta ctt tgt gat ctg gga
                                                                      192
Lys Leu Asn Lys Arg Cys Leu Pro Asn Gly Val Leu Cys Asp Leu Gly
tet eca eca tae tge tge agt gge tgg tge geg ate gte tge ate
                                                                     240
Ser Pro Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
                            70
taaaactgtc gtcatgtctt ctactcccat ctgtgctacc cctcgag
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Trp Thr Phe Val Met Ala Asp Asp Ser Arg Asn Asp Leu Glu Asn Leu
Phe Leu Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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Pro Tyr Cys Cys Ser Gly Trp Cys Ala Ile Val Val Cys Ile
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        pho-Tyr or O-phospho-Tyr; Xaa at residue 20 may be Trp or bromo-T
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Cys Ser Gly Xaa Cys Ala Ile Val Val Cys Ile
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acc gcc tgg aca ttc gtc acg gct gat gac tcc ata aat ggg ttg gag
                                                                       96
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                    20
                                         25
aat ctt ttt ccg aag gca cgt cac gaa atg agg aaa ccc gaa gcc tct
                                                                      144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Arg Lys Pro Glu Ala Ser
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Arg Ser Arg Gly Arg Cys Arg Pro Arg Gly Met Phe Cys Gly Phe Pro
                                                     60
aaa cct gga cca tac tgc tgc aat ggc tgg tgc ttt ttc gtc tgc atc
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      PRT
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Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Leu Glu Asn Leu
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Arg Gl 50	y Arg	Cys	Arg	Pro	Arg 55	Gly	Met	Phe	Cys	Gly 60	Phe	Pro	Lys	Pro	
Gly Pr 65	o Tyr	Cys	Cys	Asn 70	Gly	Trp	Cys	Phe	Phe 75	Val	Cys	Ile			
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Cys Cy	s Asn	Gly 20	Xaa	Cys	Phe	Phe	Val 25	Cys	Ile						
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acc gcc Thr Ala 15	c tgg a Trp	aca Thr	ttt Phe	gcc Ala 20	acg Thr	gct Ala	gat Asp	gac Asp	ccc Pro 25	aga Arg	aat Asn	gga Gly	ttg Leu	gag Glu 30	96
aat cti Asn Lei	ttt Phe	tcg Ser	aag Lys 35	gca Ala	cat His	cac His	gaa Glu	atg Met 40	aag Lys	aac Asn	ccc Pro	gaa Glu	gcc Ala 45	tct Ser	144
aaa tto Lys Lei	g aac 1 Asn	aag Lys 50	agg Arg	tgc Cys	cct Pro	aac Asn	act Thr 55	ggt Gly	gaa Glu	tta Leu	tgt Cys	gat Asp 60	gtg Val	gtt Val	192
gaa caa Glu Glr	aac Asn 65	tgc Cys	tgc Cys	tat Tyr	Thr	tat Tyr 70	tgc Cys	ttt Phe	att Ile	gta Val	gtc Val 75	tgc Cys	cta Leu		237
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<213> Conus lividus
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Phe Ser Lys Ala His His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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Asn Cys Cys Tyr Thr Tyr Cys Phe Ile Val Val Cys Leu
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        12 may be Glu or gamma-carboxy-Glu; Xaa at residues 17 and 19 ma
       y be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
       O-phospho-Tyr
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Xaa Thr Xaa Cys Phe Ile Val Val Cys Leu
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acc gcc tgg aca ttc gtc aag gct gat gac tcc aga aat gga ttg gag
                                                                       96
Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu
15
                    20
aat ctt ttt ccg aag gca cgt cac gaa atg aag aac tcc aaa gcc tct
                                                                      144
Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser
aaa tta aac aag agg tgc gtt gaa gat ggt gat ttt tgt ggt ccg gga
                                                                      192
Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly
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50 55 60 tat gaa gag tgc tgc agt ggc ttc tgc ctt tac gtc tgc atc 234 Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile taaaactgcc gtgatgtctt ctactcccat ctgtgctacc cctcgag 281 <210> 333 <211> 76 <212> PRT <213> Conus pulicarius <400> 333 Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Phe Leu Thr Ala Trp Thr Phe Val Lys Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu Phe Pro Lys Ala Arg His Glu Met Lys Asn Ser Lys Ala Ser Lys Leu Asn Lys Arg Cys Val Glu Asp Gly Asp Phe Cys Gly Pro Gly Tyr Glu Glu Cys Cys Ser Gly Phe Cys Leu Tyr Val Cys Ile <210> 334 <211> 25 <212> PRT <213> Conus pulicarius <220> <221> SITE <222> (1)..(25)<223> Xaa at residues 3, 13 and 14 may be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Pro or hydroxy-Pro; Xaa at residues 12 and 22 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Ty r or O-phospho-Tyr <400> 334 Cys Val Xaa Asp Gly Asp Phe Cys Gly Xaa Gly Xaa Xaa Xaa Cys Cys Ser Gly Phe Cys Leu Xaa Val Cys Ile <210> 335 <211> 293 <212> DNA <213> Conus generalis <220> <221> CDS <222> (7)..(249) <400> 335 ggatcc atg aaa ctg acg tgt gtg gtg atc gtt gct gtg cta ttc ttg Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu 48 acc gcc tgg aca ttc gtc acg gct gat gac acc aga tat aaa ctg gag 96

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Thr Ala Trp Thr Phe Val Thr Ala Asp Asp Thr Arg Tyr Lys Leu Glu
                     20
                                         25
 aat cct ttt ctg aag gca cgc aac gaa ctg cag aaa cac gaa gcc tct
                                                                       144
Asn Pro Phe Leu Lys Ala Arg Asn Glu Leu Gln Lys His Glu Ala Ser
                                     40
 caa ctg aac gag aga ggc tgc ctt gac cca ggt tac ttc tgt ggg acg
                                                                       192
Gln Leu Asn Glu Arg Gly Cys Leu Asp Pro Gly Tyr Phe Cys Gly Thr
ccg ttt ctt gga gca tac tgc tgc ggt ggc att tgc ctt att gtc tgc
                                                                       240
Pro Phe Leu Gly Ala Tyr Cys Cys Gly Gly Ile Cys Leu Ile Val Cys
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Ile Glu Thr
    80
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Thr
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       es 7 and 17 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-
       sulpho-Tyr or O-phospho-Tyr
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acc gcc tgg aca ttt gcc acg gct gat gac ccc aga aat gga ttg ggg
                                                                     96
Thr Ala Trp Thr Phe Ala Thr Ala Asp Asp Pro Arg Asn Gly Leu Gly
                    20
aat ctt ttt tcg aat gta cat cac gaa atg aag aac ctc gaa gac tct
                                                                    144
Asn Leu Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser
aaa ttg gac aag aag tgc ctt ggg ttt ggt gaa gct tgt ctt atg ctt
                                                                    192
Lys Leu Asp Lys Lys Cys Leu Gly Phe Gly Glu Ala Cys Leu Met Leu
                               55
tat tca gac tgc tgc agc tat tgc gtt gct ctt gtc tgc cta
                                                                    234
Tyr Ser Asp Cys Cys Ser Tyr Cys Val Ala Leu Val Cys Leu
taaaactacc gtgacgtctt ctactcccct ctgtgctacc tggcttgatc tttgattggc
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gtgtgcgctt cactggttat gaacccctct gatcctactc tctgaagacc tctggggtcc
                                                                    354
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Phe Ser Asn Val His His Glu Met Lys Asn Leu Glu Asp Ser Lys Leu
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<220>
<221>
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       12 and 18 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
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ulpho-Tyr or O-phospho-Tyr

ulph	o-Tyr or	O-phosp	ho-Tyr					
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Ser Xaa Cys	Val Ala 20	Leu Val	. Cys Leu 25	1				
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acc gcc tgg Thr Ala Trp 15	aca ttc Thr Phe	gtc atg Val Met 20	gct gat Ala Asp	gac ccc Asp Pro 25	aga gat Arg Asp	gaa ccg Glu Pro	gag Glu 30	96
gca cgt gac Ala Arg Asp	gaa atg Glu Met 35	aac ccc Asn Pro	gca gcc Ala Ala	tct aaa Ser Lys 40	ttg aac Leu Asn	gag aga Glu Arg 45	ggc Gly	144
tgc ctt gca Cys Leu Ala	gtt gat Val Asp 50	tat ttt Tyr Phe	tgc ggc Cys Gly 55	ata ccg Ile Pro	ttt gtg Phe Val	agc aac Ser Asn 60	gjå aaa	192
cta tgc tgc Leu Cys Cys 65	agt ggc Ser Gly	aat tgt Asn Cys	gtt ttt Val Phe 70	gtc tgc Val Cys	aca ccc Thr Pro 75	caa ggg Gln Gly	aag Lys	240
taaaactgcc q	gtgacgtc	tt ctact	cccct ct	gtgctacc	tggcttga	atc tttga	attggc	300
gtgtgcactt d	cactggtt	at gaacc	cctct ga	tcctactc	tctgaaga	acc tctg	gggtcc	360
aacatccaaa t	caaagcga	ca teccaa	aaaaa aa	aaaaaaaa	aaaa			404
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Trp Thr Phe	Val Met 20	Ala Asp	Asp Pro 25	Arg Asp	Glu Pro	Glu Ala 30	Arg	
Asp Glu Met 35	Asn Pro	Ala Ala	Ser Lys	Leu Asn	Glu Arg 45	Gly Cys	Leu	
Ala Val Asp 50	Tyr Phe	Cys Gly 55	Ile Pro	Phe Val	Ser Asn	Gly Leu	Cys	
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       r, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residues 12 and 30 may b
       e Pro or hydroxy-Pro
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Gly Leu Cys Cys Ser Gly Asn Cys Val Phe Val Cys Thr Xaa Gln
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ctctttctgt ttgtgtctaa cagg ttg aga tgg tgc att cct aga ggt gat
                                                                      111
                           Leu Arg Trp Cys Ile Pro Arg Gly Asp
ctt tgt ttc ccc tcg gat cgc ata caa tgc tgc agt ggc aag tgc aca
                                                                      159
Leu Cys Phe Pro Ser Asp Arg Ile Gln Cys Cys Ser Gly Lys Cys Thr
                    15
                                         20
ttc gtc tgc atg taaaactgcc gtgatgtctt ctcctccct c
                                                                      202
Phe Val Cys Met
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<211> 29
<212> PRT
<213> Conus achatinus
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Leu Arg Trp Cys Ile Pro Arg Gly Asp Leu Cys Phe Pro Ser Asp Arg
                                    10
Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
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<211> 27
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<220>
<221>
      SITE
<222> (1)..(27)
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       1 may be Pro or hydroxy-Pro
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Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
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       202
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ctctttctgt ttgtgtctga caga ttg aga ggg tgc gtt cct agt ggt gaa
                                                                      111
                           Leu Arg Gly Cys Val Pro Ser Gly Glu
att tgt tac ttc atg gat cac ata gga tgc tgc agt ggc aag tgc aca
                                                                      159
Ile Cys Tyr Phe Met Asp His Ile Gly Cys Cys Ser Gly Lys Cys Thr
ttc gtc tgc atg taaaactgcc gtgatgtctt ctcctcccat c
                                                                      202
Phe Val Cys Met
<210> 348
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      PRT
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      Conus achatinus
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Leu Arg Gly Cys Val Pro Ser Gly Glu Ile Cys Tyr Phe Met Asp His
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       be Glu or gamma-carboxy-Glu; Xaa at residue 10 may be Tyr, 125-Ī-
       Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
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Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
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        DNA
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                                     10
tgg aca ttc gtc acg gct gat gac tcc aca tat gga ttg aag aat ctt
                                                                        96
Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu
ttg ccg aac gga cgt cat gaa atg atg aac ccc gaa gcc cct aaa ttg
                                                                       144
Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu
                             40
aac aag aaa gat gaa tgc tct gct cct ggt gca ttt tgt ctc atc agg
                                                                      192
Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
cca gga ctc tgc tgc agc gag ttc tgc ttc ttt gcg tgt ttt
                                                                      234
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe
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tagtgacggt tgatgtcttc tactcccctc
                                                                      264
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       78
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Trp Thr Phe Val Thr Ala Asp Asp Ser Thr Tyr Gly Leu Lys Asn Leu
Leu Pro Asn Gly Arg His Glu Met Met Asn Pro Glu Ala Pro Lys Leu
Asn Lys Lys Asp Glu Cys Ser Ala Pro Gly Ala Phe Cys Leu Ile Arg
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Phe Ala Cys Phe
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      SITE
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      residues 6 and 14 may be Pro or hydroxy-Pro
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Met Lys Leu Thr Cys Val Met Ile Val Thr Val Leu Phe Leu Thr Āla
                                                                       96
tgg aca tte gte aeg get gat gae tee aga gae get eeg gat agt gea
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asp Ala Pro Asp Ser Ala
                                                                      144
gaa gga tgg gag aaa ctt ttc tcg gag gca cgt gac gaa atg aag aac
Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
cgc aaa gac ttt gaa ttg aga ggg tgc ctt cct agg tgg gaa ttt tgt
                                                                      192
Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
    50
                                                                      240
ccc atc ttt aaa aaa aac gat tgc tgc agt ggc ata tgc ata agc atc
Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
                                                                      276
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Cys Leu
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Glu Gly Trp Glu Lys Leu Phe Ser Glu Ala Arg Asp Glu Met Lys Asn
                            40
Arg Lys Asp Phe Glu Leu Arg Gly Cys Leu Pro Arg Trp Glu Phe Cys
Pro Ile Phe Lys Lys Asn Asp Cys Cys Ser Gly Ile Cys Ile Ser Ile
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Cys Leu
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       e 6 may be Trp or bromo-Trp; Xaa at residue 7 may be Glu or gamma
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tgg ata ttt gta atg gct gat gac tcc aga aat gga ttg gag aat ctt
                                                                          96
Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
                                  25
cct cag act aca cgt cac gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                         144
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
aac cag aca gac tgc ctt gct aaa gac gct ttc tgt gcc tgg ccg ata
                                                                         192
Asn Gln Thr Asp Cys Leu Ala Lys Asp Ala Phe Cys Ala Trp Pro Ile
    50
ctt gga cca ctg tgc tgc agt cgc ttg tgc tta tac gtc tgc atg
                                                                         237
Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
                     70
taaaactgcc gtgatgtctt ctactcccct c
                                                                         268
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Trp Ile Phe Val Met Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
Pro Gln Thr Thr Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
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Leu Gly Pro Leu Cys Cys Ser Arg Leu Cys Leu Tyr Val Cys Met
                    70
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      28
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tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
            20
tet eeg aag gea egt eac gaa atg aag aac eee gaa gee tet aaa teg
                                                                      144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac
                                                                      192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
                        55
gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca
                                                                      240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
                    70
                                        75
ttt tcg tgatgtcttc tcctccctc
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Phe Ser
<210> 360
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Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
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Phe Ser
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      Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
<223>
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
        Glu or gamma-carboxy-Glu
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Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
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tgg aca ttc gtc acg gct gat gac tcc aga tat gga ttg aag aat ctt
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Tyr Gly Leu Lys Asn Leu
            20
                                25
ttt ccg aag gca cgt cat gaa atg aag aac cct gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
        35
aac aag aga gat ggg tgc tat aat gct ggt aca ttt tgt ggc atc cgt
                                                                      192
Asn Lys Arg Asp Gly Cys Tyr Asn Ala Gly Thr Phe Cys Gly Ile Arg
cca gga ctc tgc tgc agc gag ttt tgc ttt tta tgg tgc ata aca ttt
                                                                      240
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Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe

75

80

289

60

112

10

cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa

gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt qgt

Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly

70

gtt gat tot ggc taacagtgtg cgttggttga tgtcttctac teccetc

65

Val Asp Ser Gly

PRT

Conus consors

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<222>

<400> 365

CDS

(83)..(175)

Conus circumcisus

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Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
                                    20
gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcttccctc
                                                                      205
Ala Phe Val Cys Leu
            30
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<213> Conus circumcisus
<400> 366
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
<210> 367
<211> 26
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<213> Conus circumcisus
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<223> Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.
<400> 367
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Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
<210> 368
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      206
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<400> 368
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gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt
                                                                      112
                         Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc
                                                                      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
                                                                      206
qca ttc qtc tqc ttq taaaactqcc gtgatgtctt ctactcccct c
Ala Phe Val Cys Leu
            30
<210> 369
<211> 31
<212> PRT
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<213> Conus circumcisus
<400> 369
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
<210> 370
<211> 27
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<223> Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
       1 may be Pro or hydroxy-Pro
<400> 370
Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
                                    10
Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
<210> 371
<211>
       206
<212>
      DNA
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      CDS
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      (83)..(175)
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cgatccatct gtccatccat ctattcattc attcgctgtc aaactgtatt aaatattcaa
                                                                       60
gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt
                                                                      112
                         Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
                                                                      160
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc agt gcc aag tgc
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys
                                    2.0
gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcctccct c
                                                                      206
Ala Phe Val Cys Leu
            30
<210> 372
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       31
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Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
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<210> 373
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Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
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<210> 374
<211> 206
<212> DNA
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      CDS
<222>
      (83)..(175)
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cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa
                                                                       60
gtctctcttt ctgttttgtgt ct aac aga ttg agt agg tgc att cct agt ggt
                                                                      112
                         Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc gag tgc
                                                                      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Glu Cys
gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctcctccct c
                                                                      206
Ala Phe Val Cys Leu
            30
<210> 375
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<213> Conus circumcisus
<400> 375
Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Gln Cys Cys Asn Ala Glu Cys Ala Phe Val Cys Leu
            20
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       376
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       26
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       PRT
<213>
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<220>
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      (1)..(26)
<222>
      Xaa at residues 3 and 10 may be Pro or hydroxy-Pro; Xaa at residu
       e 20 may be Glu or gamma-carboxy-Glu
<400> 376
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Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln Cys
Cys Asn Ala Xaa Cys Ala Phe Val Cys Leu
      377
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gtctctcttt ctgtttgtgt ct aac aga ttg agt tgg tgc att cct agt ggt
                                                                     112
                         Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
                                                                     160
gat ctt tgt ttc ccc tcg gat cac ata cga tgc tgc agt gcc aag tgc
Asp Leu Cys Phe Pro Ser Asp His Ile Arg Cys Cys Ser Ala Lys Cys
                15
gca ttc gtc tqc ttg taaaactgcc gtgatgtctt ctcttcccat c
                                                                     206
Ala Phe Val Cys Leu
            30
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<211>
       31
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Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Arg Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
<210> 379
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       1 may be Pro or hydroxy-Pro
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Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
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       206
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gtctctcttt ctgtttgtgt ct aac aga ttg agt agg tgc att cct agt ggt
                                                                      112
                         Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly
gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc
                                                                      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
gca ttc gcc tgc ttg taaaactgcc gtgatgtctt ctcttcccct c
                                                                      206
Ala Phe Ala Cys Leu
            30
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       381
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       31
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      Conus circumcisus
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Asn Arg Leu Ser Arg Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
                                 25
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      26
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       (1)..(26)
<223>
       Xaa at residues 3 and 10 may be Pro or hydroxy-Pro.
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Cys Asn Ala Lys Cys Ala Phe Ala Cys Leu
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                                 2.5
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      383
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      DNA
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       CDS
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      (83)..(175)
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cgatccatct gtccatccat ctattcattc attcgctgcc aaactgtatt aaatattcaa
                                                                       60
gtetetettt etgittgtgt et aac aga ttg agt tgg tge att eet agt ggt
                                                                      112
                         Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly
                                                              1.0
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gat ctt tgt ttc ccc tcg gat cac ata caa tgc tgc aat gcc aag tgc
                                                                      160
Asp Leu Cys Phe Pro Ser Asp His Ile Gln Cys Cys Asn Ala Lys Cys
gca ttc gtc tgc ttg taaaactgcc gtgatgtctt ctactcccct c
                                                                      206
Ala Phe Val Cys Leu
            30
      384
<210>
<211>
      31
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      PRT
<213> Conus circumcisus
<400> 384
Asn Arg Leu Ser Trp Cys Ile Pro Ser Gly Asp Leu Cys Phe Pro Ser
                                    10
Asp His Ile Gln Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
                                25
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      27
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      PRT
<213>
      Conus circumcisus
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<221>
      SITE
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       (1)..(27)
<223>
      Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residues 4 and 1
       1 may be Pro or hydroxy-Pro
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Xaa Cys Ile Xaa Ser Gly Asp Leu Cys Phe Xaa Ser Asp His Ile Gln
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Cys Cys Asn Ala Lys Cys Ala Phe Val Cys Leu
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       200
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<221> CDS
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                                                                       60
ctttctgttt gtgtct aac aga ttg agt tgg tgc att cct act ggt gat ctt
                                                                      112
                  Asn Arg Leu Ser Trp Cys Ile Pro Thr Gly Asp Leu
                  1
tgt ttc ccc tcg gat cac ata caa tgc tgc agt ggc aag tgc aca ttc
                                                                      160
Cys Phe Pro Ser Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe
                            20
gtc tgc atg taaaactgcc gtgatgtctt ctcctcccct c
                                                                      200
Val Cys Met
    30
<210> 387
<211> 31
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<212> PRT
<213> Conus circumcisus
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Asp His Ile Gln Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
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<211>
<212> PRT
<213> Conus circumcisus
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<221> SITE
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       1 may be Pro or hydroxy-Pro
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Cys Cys Ser Gly Lys Cys Thr Phe Val Cys Met
            20
<210>
      389
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       266
<212> DNA
<213> Conus monachus
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<221> CDS
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Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
                                    10
tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt
                                                                      96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
tet eeg aag gea egt eac gaa atg aag aac eee gaa gee tet aaa teg
                                                                     144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
        35
aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca
                                                                     240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
ttt tcg tgatgtcttc tcctcccctc
                                                                     266
Phe Ser
<210> 390
<211> 82
<212> PRT
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<213> Conus monachus
<400> 390
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
Phe Ser
<210> 391
<211> 31
<212> PRT
<213> Conus monachus
<220>
<221>
      SITE
       (1)..(31)
<222>
      Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
       Glu or gamma-carboxy-Glu
<400> 391
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
            20
<210> 392
<211> 277
<212> DNA
<213> Conus stercusmuscarum
<220>
<221>
      CDS
<222>
      (1)..(246)
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                                                                       48
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
                                    1.0
tgg aca ttc gtc aca gct gat gac tcc ata aat gga ccg gag aat aga
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
cga ata tgg gag aaa ctt ttg ttg aag gca cgt gac gaa atg aag aac
                                                                      144
Arg Ile Trp Glu Lys Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
ccc gaa gcc tct caa ttg aga tgg tgc att cct agt ggt gaa ctt tgt
                                                                     192
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
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ttc cgc tcg gat cac ata caa tgc tgc agt gcc aag tgc gca ttc gtc
                                                                     240
Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
                                        75
                    70
tgc ttg taaaactacc gtgatgtctt ctcctcccat c
                                                                      277
Cys Leu
<210> 393
<211> 82
<212>
      PRT
<213>
      Conus stercusmuscarum
<400> 393
Met Lys Leu Thr Cys Met Met Ile Val Ala Val Leu Phe Leu Thr Ala
                                    10
Trp Thr Phe Val Thr Ala Asp Asp Ser Ile Asn Gly Pro Glu Asn Arg
Arg Ile Trp Glu Lys Leu Leu Lys Ala Arg Asp Glu Met Lys Asn
Pro Glu Ala Ser Gln Leu Arg Trp Cys Ile Pro Ser Gly Glu Leu Cys
Phe Arg Ser Asp His Ile Gln Cys Cys Ser Ala Lys Cys Ala Phe Val
Cys Leu
<210> 394
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      27
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<213> Conus stercusmuscarum
<220>
<221>
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<222>
       (1)..(27)
       Xaa at residue 1 may be Trp or bromo-Trp; Xaa at residue 4 may be
<223>
       Pro or hydroxy-Pro; Xaa at residue 7 may be Glu or gamma-carboxy
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Xaa Cys Ile Xaa Ser Gly Xaa Leu Cys Pro Arg Ser Asp His Ile Gln
Cys Cys Ser Ala Lys Cys Ala Phe Val Cys Leu
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       395
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       266
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<221> CDS
<222>
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                                                                       48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
                                    10
                                                        15
tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg aag aat ctt
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96

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Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
                                 2.5
ttt ccg aag gca cgt cat gaa atg aag aac ccc gaa gcc tct aaa ttg
                                                                      144
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
                             40
aac aag aga gat ggg tgc tct agt ggt ggt aca ttt tgt ggc atc cgt
                                                                      192
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
cca gga ctc tgc tgc agc gag ttt tgc ttt ctt tgg tgc ata aca ttt
                                                                      240
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
                                         75
att gat tgatgtcttc tattcccctc
                                                                      266
Ile Asp
<210> 396
<211> 82
<212> PRT
<213>
       Conus stercusmuscarum
<400> 396
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Ile Ala
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Lys Asn Leu
Phe Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Leu
Asn Lys Arg Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg
Pro Gly Leu Cys Cys Ser Glu Phe Cys Phe Leu Trp Cys Ile Thr Phe
Ile Asp
<210> 397
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       31
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<213> Conus stercusmuscarum
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<221>
      SITE
<222>
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<223> Xaa at residue 14 may be Pro or hydroxy-Pro; Xaa at residue 20 ma
       y be Glu or gamma-carboxy-Glu; Xaa at residue 25 may be Trp or br
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Asp Gly Cys Ser Ser Gly Gly Thr Phe Cys Gly Ile Arg Xaa Gly Leu
Cys Cys Ser Xaa Phe Cys Phe Leu Xaa Cys Ile Thr Phe Ile Asp
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<210>
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<211> 265
<212> DNA
<213> Conus striolatus
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                                                                        48
 Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala
                                     10
 tgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt
                                                                        96
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
                                 25
ctt ctg aag aca cgt cac gaa gtg gaa aac ccc aaa gcc tct agg tcg
                                                                       144
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
ggc ggt agg tgc cgt cct ggt ggt acg gtt tgt ggc ttt ccg aaa cct
                                                                       192
Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
gga cca tac tgc tgc agt ggc tgg tgc ttt ttt gtc tgc gcc
                                                                      234
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
taaacctgcc gtgatgtctt ctcctcccat c
                                                                      265
<210> 399
<211> 78
<212> PRT
<213> Conus striolatus
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Met Lys Leu Thr Cys Ile Met Thr Val Ala Val Leu Phe Leu Thr Ala
Trp Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
Leu Leu Lys Thr Arg His Glu Val Glu Asn Pro Lys Ala Ser Arg Ser
Gly Gly Arg Cys Arg Pro Gly Gly Thr Val Cys Gly Phe Pro Lys Pro
Gly Pro Tyr Cys Cys Ser Gly Trp Cys Phe Phe Val Cys Ala
<210> 400
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       27
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       PRT
<213>
      Conus striolatus
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<222>
       (1)..(27)
      Xaa at residues 3, 11, 13 and 15 may be Pro or hydroxy-Pro; Xaa a
       t residue 16 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O
       -sulpho-Tyr or O-phospho-Tyr; Xaa at residue 21 may be Trp or bro
       mo-Trp
<400> 400
Cys Arg Xaa Gly Gly Thr Val Cys Gly Phe Xaa Lys Xaa Gly Xaa Xaa
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Cys Cys Ser Gly Xaa Cys Phe Phe Val Cys Ala
 <210> 401
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 <212>
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        Conus striolatus
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       (1)..(243)
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                                                                       48
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
 tgg aca ttc gtc acg gct gat gac tcc aaa aat gga ctg gag aat cat
                                                                       96
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
             20
ttt tgg aag gca cgt gac gaa atg aag aac cgc gaa gcc tct aaa ttg
                                                                      144
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
        35
gac aaa aag gaa gcc tgc tat ccg cct ggt act ttt tgt ggc ata aag
                                                                      192
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
    50
ccc ggg cta tgc tgc agt gag ttg tgt tta ccg gcc gtc tgc ggt
                                                                      240
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
ggt taactgccgt gatgtcttct attcccctc
                                                                      272
Gly
<210> 402
<211> 81
<212> PRT
<213> Conus striolatus
<400> 402
Met Lys Leu Thr Cys Val Met Ile Val Ala Val Leu Phe Leu Thr Ala
Trp Thr Phe Val Thr Ala Asp Asp Ser Lys Asn Gly Leu Glu Asn His
Phe Trp Lys Ala Arg Asp Glu Met Lys Asn Arg Glu Ala Ser Lys Leu
Asp Lys Lys Glu Ala Cys Tyr Pro Pro Gly Thr Phe Cys Gly Ile Lys
Pro Gly Leu Cys Cys Ser Glu Leu Cys Leu Pro Ala Val Cys Val Gly
Gly
<210> 403
<211> 29
<212>
      PRT
<213> Conus striolatus
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<220>
 <221>
        SITE
 <222>
        (1)..(29)
 <223>
        Xaa at residues 1 and 20 may be Glu or gamma-carboxy-Glu; Xaa at
         residue 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-s
        ulpho-Tyr or O-phospho-Tyr; Xaa at residues 5, 6, 14 and 24 may b
        e Pro or hydroxy-Pro
 <400> 403
Xaa Ala Cys Xaa Xaa Gly Thr Phe Cys Gly Ile Lys Xaa Gly Leu
 Cys Cys Ser Xaa Leu Cys Leu Xaa Ala Val Cys Val Gly
<210>
       404
<211>
       265
<212>
       DNA
<213>
       Conus striolatus
<220>
<221>
       CDS
<222>
       (1)..(246)
<400> 404
atg aaa ctg acg tgt ctg atg gct gtt gct gtg ctg ttc ttg acc gcc
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
cgg aca ttc gtc acg gct gat gac tcc aga aat gga ttg gag aat ctt
                                                                       96
Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
tct ccg aag gca cgt cac gaa atg aag aac ccc gaa gcc tct aaa tcg
                                                                      144
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
aac aag aga tat gag tgc tat tct act ggt aca ttt tgt ggc atc aac
                                                                      192
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
gga gga ctc tgc tgc agc aac ctt tgc tta ttt ttc gtg tgc tta aca
                                                                      240
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
ttt tcg tgatgtcttc tatcccctc
                                                                      265
Phe Ser
<210> 405
<211>
      82
<212>
       PRT
<213>
      Conus striolatus
<400> 405
Met Lys Leu Thr Cys Leu Met Ala Val Ala Val Leu Phe Leu Thr Ala
                                    10
Arg Thr Phe Val Thr Ala Asp Asp Ser Arg Asn Gly Leu Glu Asn Leu
Ser Pro Lys Ala Arg His Glu Met Lys Asn Pro Glu Ala Ser Lys Ser
                            40
Asn Lys Arg Tyr Glu Cys Tyr Ser Thr Gly Thr Phe Cys Gly Ile Asn
```

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50
                          55
                                               60
Gly Gly Leu Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr
                                           75
Phe Ser
<210> 406
<211> 31
<212> PRT
<213> Conus striolatus
<220>
<221>
       SITE
<222>
       (1)..(31)
<223> Xaa at residues 1 and 4 may be Tyr, 125-I-Tyr, mono-iodo-Tyr, di-
       iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 2 may be
       Glu or gamma-carboxy-Glu
<400> 406
Xaa Xaa Cys Xaa Ser Thr Gly Thr Phe Cys Gly Ile Asn Gly Gly Leu
Cys Cys Ser Asn Leu Cys Leu Phe Phe Val Cys Leu Thr Phe Ser
<210> 407
<211>
       287
<212>
       DNA
<213>
       Conus striolatus
<220>
<221>
      CDS
<222>
       (1)...(231)
atg aaa ctg acg tgt atg gtg atc gtc gcc gtg ctg ctc ctg acg acc
Met Lys Leu Thr Cys Met Val Ile Val Ala Val Leu Leu Leu Thr Thr
                                                                           48
                                      10
tgt cat ctc atc aca gct gat gac tcc aga ggt acg cag aag cat cgt
                                                                           96
Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg
             20
tcc ctg agg tcg act acc aaa gtc tcc aag tcg act agc tgc atg aaa
                                                                          144
Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys
        35
                              40
gee ggg tet tat tge gte get act acg aga ate tge tge ggt tat tge
                                                                         192
Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys
    50
                         55
gct tat ttc ggc aaa ata tgt att ggc tat ccc aaa aac tgatcctccc
                                                                         241
Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn
cctactgtgc tctatccttt tctgcctgat gtcttctcct cccctc
                                                                         287
<210>
       408
<211>
       77
<212> PRT
<213> Conus striolatus
<400> 408
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Cys His Leu Ile Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Arg $20 \hspace{1.5cm} 25 \hspace{1.5cm} 30$

Ser Leu Arg Ser Thr Thr Lys Val Ser Lys Ser Thr Ser Cys Met Lys 35 40 45

Ala Gly Ser Tyr Cys Val Ala Thr Thr Arg Ile Cys Cys Gly Tyr Cys 50 55 60

Ala Tyr Phe Gly Lys Ile Cys Ile Gly Tyr Pro Lys Asn 65 70 75

<210> 409

<211> 35

<212> PRT

<213> Conus striolatus

<220>

<221> SITE

<222> (1)..(35)

<223> Xaa at residues 10, 21, 24 and 32 may be Tyr, 125-I-Tyr, mono-iod o-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr; Xaa at residue 33 may be Pro or hydroxy-Pro

<400> 409

Ile Cys Cys Gly Xaa Cys Ala Xaa Phe Gly Lys Ile Cys Ile Gly Xaa 20 25 30

Xaa Lys Asn 35